\$TIC-Biotech/ChemLib

From: Sent:

Schnizer, Richard Monday, March 10, 2003 12:11 PM STIC-Biotech/ChemLib 09/836,439

To:

Subject:

Please search the commercial databases for SEQ ID NOS: 1-6 from 09/836,439.

Thank you-

Richard Schnizer, Ph.D. Patent Examiner
Art Unit 1635
CM1 12E17
703-306-5441
Mail Box CM1 11E12

Point of Contact: **Toby Port** Technical Info. Specialist CM1 6A04 703-308-3534

Searcher:
Phone:
Location:
Date Picked Up: 3/11
Date Completed: 3/19
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

ENDOR/COST (where applic.)
STN:
DIALOG:
uestel/Orbit:
ORLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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REFERENCE AUTHORS TITLE JOURNAL FEATURES

Unknow...
Unclassified.
1 (bases 1 to 68)
1 (bases 1 to 68)
Kmlec, E. B.
Chimeric mutational vectors having non-natural nucleotides
Patent: US 5795972-A 23 18-AUG-1998;
Patent: US cation/Qualifiers

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

KEYWORDS SOURCE ORGANISM	RESULT 1 AR024440 LOCUS DEFINITION ACCESSION VERSION		4.4 4.5	43	4 3 1	40	ນ ພ ຍ 8	c 37		334			a c 30		227	c 26		2 2 3	22	20	19		c 16	L1 L4	13	c 12	c 10		ω ~	c 3 6		n د 4	2 ;	_ : _ :	Result No.	
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                                                                                                                                                 This sequence was identified as CDM:10212153 by the submitter. For more information on this record e-mail to fly@celera.com.
                                                                                                                                                                                           Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 10591)
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                                                                                                                                                                                                                                           For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www-hgc.lbl.gov/sequence-archive.html) or send email to drosophila@genome.lbl.gov.

This Pl was assembled from the following subclones: 2_cl
(AC001994), 2_bl2 (AC002947), 1_g6 (AC002944), 1_d4 (AC002943),
2_b5, 2_e4 (AC002952), 1_b4, 2_a1, 2_a2, 1_b6 (AC001992), 1_b8
(AC002945), 2_a8 (AC002946), 1_b2 (AC001994), 2_cc (AC001993), 2_d5
(AC002945), 1_b3 (AC001991), 1_d3 (AC002942), 2_a9 (AC001993),
2_c10 (AC002948), 2_g9 (AC002953), 1_g7 (AC001990), 1_b5
(AC001989), 2_c3 (AC002949), 2_h2, 2_c4 (AC002950), 2_b6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celniker, S.E., Aghavani, A., Arcaina, T.T., Baxter, E., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Ko, C.L., Li, M., Lomotan, M.A., Mazda, P., Mok, M.S., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, D., Santos, R.F., Snir, E., Stevko, V., Subramanian, S., Towne, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker,S.E., Aghavani,A., Arcaina,T.T., Baxter,E., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Ko,C.L., Li,M., Lomotan,M.A., Mazda,P., Mok,M.S., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Punch,D., Santos,R.F., Snir,E., Stevko,V., Subramanian,S., Towne,B.,
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AC003055 AC001994 AC002947 AC002944 AC002943 AC002952 AC001992
AC002945 AC002946 AC001988 AC001995 AC002951 AC001991 AC002942
AC001993 AC002948 AC002953 AC001990 AC001989 AC002949 AC002950
AC003055.1 GI:2584828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-NOV-1997) Berkeley Drosophila Genome Project, N
74-157, Lawrence Berkeley National Laboratory, One Cyclotron
Berkeley, CA 94720, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kimmel, B.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing of Drosophila chromosome 2L, region 22F Unpublished (1997)
2 (bases 1 to 73076)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC003055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lawrence Berkeley National Laboratory, MS 74-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berkeley Drosophila Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kimmel, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Subclones in pOT2 from P1 clone DS06332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (D91))
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                                                                                                         /organism="Drosophila melanogaster'
/db_xref="taxon:7227"
/chromosome="2L"
                          /clone="P1 DS06332 (D91)"
14890 c 15769 g 21214
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                       .73076
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73076 bp
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COMMENT
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Best Local Similarity
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Reference of the companies of th
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                                                                                                                                                                                                                                                               shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-JUN-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Rc Berkeley, CA 94720, US
On Sep 6, 2001 this sequence version replaced gi:14550291.
                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was assembled using end sequences from a whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence submitted by:
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2 (bases 1
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1 (bases 1 to 168540)
Celniker, S. E., Adams, M.D., Kronmiller, B.,
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/organism="Drosophila melanogaster"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                                                                     Location/Qualifiers
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Pred. No. 14;
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REFERENCE
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Addams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Andams, M.D., Celniker, S.E., Li, P.W., Hoskins, R.A., Galler, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Péalféer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Beson, K.Y., Barndale, J., Bayraktaroglu, L., Beasley, E.M., Beeson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Ballew, R.M., Beson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bottler, P., Burtis, K.C., Cherry, J.M., Cawley, S., Dahlke, C., Detter, A., Chandra, I., Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Duetz, S. M., Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandra, S., Dunkoy, B.C., Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Duetz, S. M., Dodson, K., Doup, L.E., Downes, M., Dugan, Rocha, S., Dunkoy, B.C., Peristera, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N. S., Howland, T.J., Harvey, D., Helman, T.J., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Well, M. H., Degwam, C., Jalali, M., Kalush, F., Karpen, G. H., Ke, Z., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Kennison, J.A., Ketchum, K.A., Klumel, B.E., Ködira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Nusskern, D.R., Nelson, D.R., Nelson, M., Niton, K., Sunger, C., Mitshian, N.V., Mobarry, C., Morris, J., Moshrefila, N., Menders, R., Sunger, Sunger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 TACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE003583 303356 bp DNA linear INV 04-OCT-20 Drosphila melanogaster genomic scaffold 142000013386046 section
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 16, complete sequence.
AE003583 AE002638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47514 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Clone="BACR34M11 (D1362)"
/Clone=lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACe3.6)"
a 37192 c 36097 g 47737 t
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/map="22E-22F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanogaster
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Pred. No. 15;
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COMMENT
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TITLE
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On Oct 9, 2000 this sequence version replaced gi:7295946.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10731132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGQQAAAPPQFGAPQPGYPGQQPGYPPQPGQQPMFGYPPQFGQQLGGPGYPPQPGAGF
PGQPGRPGFNQPPMPGAGNMYQQAPQARRLDPDQMPDFYQYMIDWRLSGGPFYYNQP
GLLPPLYTTKFYVHDQGKSSRPEILRSGLYCLTURTGDLLKTTALPLTLAUSPLAKYGGE
EMEPPINNFGEMGPIRCNRCKAYMSPNNQFVDAGRRFQCLMCKVTSEVHQNYYQHLDH
TGQRVDKHERPELLLGTYEFLATKDYCRNNTPPEVPAFIFIIDVSYNTVKSGLVHLLC
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/db_xref="FLYBASE:FBan0031408"
/db_xref="FLYBASE:FBgn0031408"
complement(join(971. .1111,1167. .1970,2033. .2900
complement(join(971. .1111,1167. .1970,2033. .2900
3158. .3273,3332. .3791,3851. .4822,5231. .5749))
/gene="CG10882"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="FLYBASE:FBan0010882"
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complement(j01n(987 ..1111,1167 ..1970,2033 ..290)
3158 ..3273,3332 ..3791,3851 ..4822,5231 ..5464))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mnpnmygppptgcqqqqggapppnsggmppqqqqlpqqqppqq
qlppqqqqqqpqygappptsaasqpylngnyqqqlatsmgglsyggggganplkppl
pqgapaaabppptgfmqfnsnaappptnnnnaafgappptqagsyyngalppssytqqs
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/db_xref="FLYBASE:FB900031404"
complement(join(6055. .6897,6960. .70
7911. .8051,8115. .8293,8640. .9191))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(<6055. .>9191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIQEILSMDLNQSVSYLYPREIPIHNVVPEETDLPTPVRCTHEKTQEDGAYILENGVH
LFVWLGQALSPDFVQSVFGVQGLQQIALERFNIVPETPLAKRIHGILEQIMKERSRYM
RVRICNNLVAAERQTGERVPTLPRGGPRYRRFRQLRGFPVSHAQGD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSAGIRPTEFYGHFFMSNTTDVELASIDATKSISIEIKHDDKLAPEENVYLQVALLYT
SCSGQRRLRILNLALRVTTTIADVFKCCDLDAMMLFFAKQACFKLMEHSPKQVKDNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FNNAYIDLATIGQVSRLTGGEVFKYTYFQADVDGKRLIQDIIKNVSRPIAFDAVMRVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQIKNILKHLPVDQGQDKSKVRVGFITYNSTVHFYNIKSSLAQPQMMVVGDVQEMFMP
LLDGFLCHPEESAAVIDALMEEIPRMFADTKETETILYPAIQAGLEALKASNAAGKLL
VFNSTLPIAEAPGKLKNRDDRKLLGTDKEKTVLTPQTTAYNTLGQECVQQGCSVDLFV
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/db_xref="FLYBASE:FBan0010882"
/db_xref="FLYBASE:FBgn0031408"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="CG10882 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="CT30485"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="2L"
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/db_xref="FLYBASE:FBan0017006"
/db_xref="FLYBASE:FBgn0031404"
/translation="MKYGFPSTNDITINETFDFVTSFDRRNSAILWMCERVDLSNRVV
                                                                                      /protein_id="AAF51282.1"
/db_xref="GI:7295984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="CG17006"
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                                                                                                                                                                                                                                                                                                                                                         /gene="CG17006"
                                                                                                                                                /codon_start=
                                                                                                                                                                            /note="CG17006 gene product"
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NVNYYEYAKTVEDMGALLAELVRYLNQEANMHYDDVYVIGHSLGAQIAGSAGKQIMPY
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AYTGSIYLPRELKSNSWFLEFQSEERTMVAVPTHFFKILVIDKKFAGDTIPYAEAYSP
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complement(<19456. .>20193)
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IPKNGTFYVKTYSKPPYAMGHRWQTEPPPREDDIENSTEE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="CG4267"
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                                                                                                                                                                                    /product="CT30489"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKTSVKILDPNVCKRSYQYITKTMICAAALLKDSCHGDSGGPLVSGGQLVGIVSYGIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Ser12 gene product; Nucleotide sequence of the Selera sequence differs from the published sequence for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Nucleotide sequence of the Celera sequence differs from the published sequence for this transcript."
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2 (bases 1 to 3554)

Scott, M. P. and Weiner, A. J.

Structural relationships among genes that control development:

sequence homology between the Antennapedia, Ultrabithorax, and

fushi tarazu loci of Drosophila

Proc. Natl. Acad. Sci. U.S.A. 81 (13), 4115-4119 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 3554)
Laughon, A. and Scott, M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence homology to Antp and Ubx genes; see DMANTP1 and DMANTP2 sequence homology to prokaryotic and pot, yeast DMA-binding domainer to pabo C.O., Sauer R.T. (1984) A. Rev. Biochem. 53, 293-32 Data kindly reviewed (19-FEB-1986) by A. Laughon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of a Drosophila segmentation gene: protein structure homology with DNA-binding proteins Nature 310 (5972), 25-31 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA binding protein; inverted repeat; segmentation unidentified reading frame.
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                                                                                                                                                                                                                                                                                                                                                                   /note="unidentified reading
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
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Pred. No. 15;
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                                                                                                                                                                                                                                               Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10210082 by the submitter. For further information on this sequence you may e-mail to
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 56043)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                            fly@celera.com.
* NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC012761
                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                              Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC012761.1 GI:6223082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                     This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                        16447
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                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
a 11385 c 11452 g 16759 t
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2862..2867
/note="pot.
a 952 c
                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="mutation ftz (Rp1) causing 10 novel amino acids and a premature stop codon (2140-2142)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSSAVSQEINHRIVTAPNGAGDFNWSHIEETLASDCKDSKTROTYTRYQTLELEKEF
HFNRYITARRRIDIANALSSERQIKIWFQNRRWKSKKDRTLDSSPEHCGAGYTAMLP
PLEATSTATGAPSVPVMYHHQTTAAYPAYSHSHGYGLLNDYPQOQTHQQYDAY
PQQYQQQCSYQQHPQDLYHLS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"pot. DNA-binding domain of the ftz protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1933. .2121

**Roote="region with homology to Antp and Ubx genes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="pot.
                                                                                                                              .56043
 39.7%;
58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alternate translation start site for ftz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyadenylation signal"
831 g 792 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyadenylation signal"
Score 27; DB Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27; DB 3; Length 3554; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56043 bp DNA linear
r, *** SEQUENCING IN PROGRESS
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                   Length 56043;
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Best Local Similarity

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  BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                         archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. pl library location: 83-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US Berkeley, CA 94720, US On or before Apr 16, 1999 this sequence version replaced gi:483986 gi:1945589, gi:1103946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martin,C.H., Arcaina,T.T., Bondoc,M.M., Chiang,A., Critz,P.A.,
Davis,C.A., Doyle,C.M., Ericsson,C.L., Farfan,D.E., Gunning,K.M.,
Houston,K.A., Jaklevic,M.A., Kadner,K.E., Kim,K., Kim,S.F.,
Ko,C.L., Lewis,K.D., Li,M., Lindquist,K.J., Lomotan,M.A.,
Lustre,V.M., Machrus,M.U., Mayeda,C.A., Miguel,T.M., Miller,C.A.,
Mok,M.S., Pacleb,J.M., Patel,S.G., Santos,R.F., Subramanian,S.,
Wan,K.H., Whitelaw,K.R., Yee,A., Yeh,R.T., Yu,C. and Palazzolo,M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
2 (bases 1 to 66991)
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1 (bases 1 to 66991)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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AC001653 L49396 L39779 L32657 L32652 L32645 L32656 L32649 L32648 L32637 L39749 L32654 L32639 L32647 L32642 L32635 L32653 L32651 L32636 L32654 L32634 L32646 L32650 L32636 L32643 L32644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and relationship to other sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence submitted by:
Berkeley Drosophila Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-APR-1997) Berkeley Drosophila Genome Project, MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berkeley, CA 94720
     19565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              further information about this sequence, including its location
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     a
                                                     /clone="P1 D807876 (D14)" /clone="P1 D807876 (D14)" /clone_lib="P1 library, partial Sau3A in pNS582tet14Ad10" /note="This sequence has not changed since its original submission on 08/25/1997. It was resubmitted in order to include all secondary accession numbers for the subclones
belonging to this clone."
1 13581 c 13571 g 20274
                                                                                                                                                                                                          /map="84B1-84B2"
                                                                                                                                                                                                                                        /chromosome="3R"
                                                                                                                                                                                                                                                                                           /strain="y2; cn bw sp"
                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
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AC101196
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                           sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                           will be sequenced to completion. In the event that
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This record contains 93 individual
                                                             the record is updated, the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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13491 13590: gap of 100 bp 11 length 14294 14393: gap of 100 bp 15200 15199: contil of 703 bp in length 15200 15099: contil of 706 bp in length 15210 15199: gap of 100 bp 15210 15199: gap of 100 bp 16109: gap of 16109: gap of 16100 bp 16100 bp 16109: gap of 161000 bp 1610000 bp 1610000 bp 1610000 bp 1610000 bp 161000 bp 1610000 bp 1610
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-4: gap of 100 bp
100 bp
3917: contig of 703 bp
4018: 4017: gap of 100 bp
4728: contig of 711 bp in
4729: 4828: gap of 100 bp
4829: 5529: contig of 70°
5530: 5639: gap of 100 bp
632: contig of 70°
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6332: contig of 70°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 705: contig of 705 bp in length
706 805: gap of 100 bp
1518 1617: gap of 100 bp
1518 2316: contig of 699 bp in length
2317 2416: gap of 100 bp
2317 2416: gap of 698 bp in length
                                                                                                                                                                                                                                                                         100 bp
25499: 9ap of 100 bp 1
25499: 9ap of 100 bp
26187: contig of 688 bp in
26287: gap of 100 -
26993: con+'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56: gap of 100 bp
22217: contig of 661 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8682: contig of 705 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of 100 bp in length gap of 100 bp in length
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377: contig of 710 bp in length
gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         698 bp in length
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                                          Дb
                                                                                                                                                                                Matches
                                                                                                                                                                                                                       Query Match
Best Local
29154 AAAGTTATTACTTTCAGCCAGGCAGGGTGAAAAGGCACGTATT 29112
                                                                     21 AAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTT 63
                                                                                                                                                                                                           Local
                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42104 42203: gap of 100 bp
42204 42906: contig of 703 bp in length
42907 43006: gap of 100 bp
43694 43793: gap of 100 bp
44595 44594: gap of 100 bp
45292 45391: gap of 100 bp
46101 46200: gap of 100 bp
46101 46200: gap of 100 bp
46101 46200: gap of 100 bp
46101 46201: gap of 100 bp
46897 46996: gap of 100 bp
46897 46996: contig of 696 bp in length
4697 46986: contig of 696 bp in length
4697 46986: contig of 696 bp in length
4697 46986: contig of 696 bp in length
46987 46981: contig of 698 bp in length
47683 47782: gap of 100 bp
48581 48580: gap of 100 bp
49289: contig of 698 bp in length
49289: contig of 698 bp in length
49389 49388: gap of 100 bp
50071 50171; gap of 100 bp
50075 5074: gap of 100 bp
51684 51783: gap of 100 bp
51684 51783: gap of 5100 bp
51684 51783: gap of 100 bp
51685 52595: gam of 100 bp
51686 52595: gam of 100 bp
51687 50976: contig of 709 bp in length
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                       52496 52595; gap of 100 bp 52596 53300; contig of 705 bp in length 53301 53400; gap of 100 bp 54108; contig of 708 bp in length 54209 54904; contig of 506 bp in length 54209 54904; contig of 506 bp in length
                                                                                                                                                                                                                                                                                                54209 54904: cont
54905 55004: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41296; conti.
41297 41396; amr
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39788 405(
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35036 35743: contig of 708 bp in length
35744 35843: gap of 100 bp
35844 36513: contig of 670 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38220 38895:
38896 38995: ga
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32568 32667: gap of 100 b
32668 33368: contig of 701
33369 33468: gap of 100 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30191 30290: gap of 100 bp
30291 30996: contig of 706 bp
30997 31096: gap of 100 bp
31097 31797: contig of 701 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31798 31897:
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41296: contig of 695 bp
1396: gap of 100 bp
42103: contig of 707 bp
2203: qap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp
1897: contig of 701 bp
1897: gap of
32567: contig
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187: gap of 100 bp
40501; contig of 714 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36513: contig of 670 bp in length 513: gap of 100 bp in length 37323: contig of --
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                                                                                                                                                                                                Score 27; DB 2; Length 74026; Pred. No. 17;
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contig of 677 bp in length
                                                                                                                                                  Mismatches
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26188 26287:

0

Gaps

0

24611 24710: 25400 25499:

23825 23924:

24610: ~

23026 23125; as

17: gap of 100 bp 23025: contig of 708 bp 25: gap of 100 bp 23824: contig of 699 bp

2218 22317:

m × < >

ULBR

	COMMENT	JOURNAL	TITLE	TITLE JOURNAL REFERENCE AUTHORS	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 11 AC012649 LOCUS DEFINITION
archive Web site (http://www.intractives.com.) to bdgp@fruitfly_berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases. the following cutoffs: length >= 200 bases. the following cutoffs: length >= 200 bases. to six so fill contigs. The true order of the pieces consists of 101 contigs. The true order of the pieces arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are runknown. the saxet sizes of the gaps are unknown. this record will be updated with the finished sequence this record will be updated with the finished sequence that soon as it is available and the accession number will the preserved. 577. contig of 577 bp in length 578. 1405. 1484: gap of unknown length 1405. 1484: gap of unknown length 1405. 2313: contig of 737 bp in length 1323: gap of unknown length 13234 2333: gap of unknown length 132331: contig of 829 bp in length 1323 3711: gap of unknown length 1320 3799: gap of unknown length 1320 3799: gap of unknown length 1320 4897: contig of 1098 bp in length 1320 4897: gap of unknown length 1320 5899: contig of 1098 bp in length 1320 5899: contig of 820 bp in length 1320 5899: contig of 820 bp in length 1320 5899: contig of 820 bp in length 1320 5899: contig of 830 bp in length 1320 5899: contig of 890 bp in length 1320 5890 5899: contig of 890 bp in length 1320 5890 5899: contig of 890 bp in length 1320 5890 5899: contig of 890 bp in length 1320 5890 5890 5890 5890 5890 5890 5890 589	on Nov 4, 1999 the sequence including its location for further information about this sequence, including its location for further information about this sequences, please visit our sequence and relationship to other sequences, please visit our sequence and relationship to other sequences, please visit our sequence.	Submitted (02-NOV-1999) Drosophila Genome Centet, Lawrence Submitted (02-NOV-1999) Brosophila Genome Centet, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA	Kim, E. Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, F., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, F., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Moshrefi, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Pieren, L., Spirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Suriskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M. Direct Submission	Unpublished Unpublished 2 (bases 1 to 80866) 2 (bases 1, Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Butenhoff, C., Champe, M., Chavez, C., George, R.A., Harris, N.L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Karra, K., Kearney, L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,	1 (bases 1 to 80000) Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Boyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Doyle, C.M., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacaleb, J.M., Park, S., Pfeiffer, B., Moshrefi, M., Nixon, K., Svirskas, R.R., Wan, K.H., Webster, D., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Richards, S., Sethi, H., Raccab, J.M., Yu, C. and Rubin, G.M.	ACO12649.2 G1:6226990 ACO12649.2 G1:622690 ACO126490 ACO	AC012649 AC012649 BO866 bp DNA linear HTG 04-NOV-1999 Drosophila melanogaster chromosome X clone BACR07N08 (D1121) RPCI-98 07.N.8 map 17D-17E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 101 unordered pieces.
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WPCOMMENT
   Sequence split into 5 fragments LOCUS AE001572 Accession AE001572
                                                                                                             Matches
Fragment Name
                                                                          15 TAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCG 65
                                                                                                                      Local
                                                               TIGCATAAAGTTTTTACTGTTTACTAGTCATTTTGGAAGTGCGTTTGTTGG 25561
                                                                                                                     Similarity
                                                                                                                                                   60452
61002
61082
61657
61657
62262
62342
62366
62346
63539
64137
                                                                                                            Conservative
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59610
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60372
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45915
45995
46590
46670
Begin
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58.8%;
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                                                                                                                                                      contig of 593 bp in length
gap of unknown length
contig of 518 bp in length
                                                                                                                                                                                                 gap of contig
                                                                                                                                                                                                                           gap of unknown length contig of 575 bp in la gap of unknown length
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                                                                                                                                                                                                                gap of unknown length contig of 525 bp in length
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gap of
contig
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contig of 727 bp
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                                                                                                                          Score 27;
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                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                        f unknown length
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of 550 bp in
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of 734 bp in
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of 432 bp in length
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of 543 bp in
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of 615 bp in
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of 361 bp in length
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jof 553 bp
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Reclinker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dletz, S. M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Dodson, K., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Parasas, V., Park, S., Patel, S., Pétifer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Niroch C., Nanissic, S.M., Richards, S., Smith, H.O., Rubin, G.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                    Berkeley Drosophila Ğenome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-SEP-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US
Sequence submitted by:
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barren, B., Barran, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Canareta, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Bagas, D., Bardyna, S., Faro, S., Ginde, S., Gordon, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S., Faro, S., Ginde, S., Gordon, S., Holme, W., Iliev, I., Johnson, R., Jones, C., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Ramat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., MacGean, C., MacCeann, C., Navior, J., Menuels, L., Mihova, T., Norbu, C., Norbu, C., NacCearthy, M., Matthews, C., McCarthy, M., Malenga, V., Murphy, T., Naylor, J., Menuels, L., Mihova, T., Norbu, C., Norbu, C., Nocola, R., Worbu, C., Nicol, R., Worbu, C., Nicol, R., Worbu, C., Nicol, R., Worbu, C., Norbu, C., Rogov, P., Roman, J., Retta, R., Ribey, C., Rogov, P., Roman, J., Severy, P., Spencer, B., Stange-Thoman, N., Stojanovic, N., Stojanovic, N., Subramanian, A., Travis, N., Trijgilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Viel, R., Norbu, C., Milson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Viel, R., Shanoun, J., Zembek, L., Zimmer, A., and Zody, M.
Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 208375)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barren,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Hagos,B., Gardyna,S., Graham,L., Grand-Pierre,N., Hagos,B., Gardyna,S., Graham,L., Johnson,R., Jones,C., Kamat,A.,
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Birren, B., Nusbaum, C.
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Mus musculus clone RP23-472H1, WORKING DRAFT SEQUENCE, 8 ordered
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                                                                                                                                                                                                                                                                                                                       Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI in pBACE3.6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="3R"
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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FEATURES
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* consists of 8 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession on the replaced

* the accession of 3805; gap of 100 bp

* 53806 53905; gap of 100 bp

* 53906 53905; gap of 100 bp

* 53906 53905; gap of 100 bp

* 53906 53905; gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
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138341 186299: contig of 47959 bp in length
186300 186399: gap of 100 bp
186400 208375: contig of 21976 bp in length.
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84267 138240: contig of 53974 bp in length
vector_side:left"
                                                                 clone_end:SP6
                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="RP23-472H1"
                                                                                                                                   /note="assembly_fragment
                                                                                                                                                                                                                                        /clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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    Summary Statistics

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Best Local Similarity
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         ORS Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Adams, M.D., Celniker, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Burner, G.G., Wortman, J.R., Yandell, M.D., Zhang, C., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazel, R.G., Champe, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Beeson, K.Y., Bensendale, J., Bayraktaroglu, L., Beasley, E.M., Beeson, K.Y., Bensendale, J., Burkats, C.J., Brottier, P., Burtis, K.C., Champe, M., Buller, H., Cadleu, E., Center, A., Chandra, I., Charle, P., Burtis, K.C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C., Pleischmann, W., Fosler, C., Gobriellan, A.E., Garg, N. S., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Wei, M.H., Ibeywam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Leits, J., Mohard, T.J., Mattel, B., McIntosh, T.C., Mortis, J., Moshrefi, A., Mount, S.M., Mattel, B., McIntosh, T.C., McLeod, M.P., McPherson, D. L., Merson, D. R., Nelson, K.A., Nixon, K., Sun, E., Son, H., Shue, B.C., Siden-Klamos, I., Sanders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Klamos, I., Sanders, R.D., Scheeler, F., Shen, H., Shue, B.C., Starling, A.C., Turner, R., Shapleton, M., Stopski, M.P., Smith, T., Spier, E., Spradling, A.C., Turner, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 AAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa: Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genomic scaffold 142000013386040 section 3 of 5, complete sequence.
AE003673 AE003699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
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.38341. .186299
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Pred. No. 18;
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On oct 9, 2000 this sequence version replaced g1:7298860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                          /note="Nucleotide sequence of the Celera sequence differs from the published sequence for this transcript."
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/gene="Scr"
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GQQLQELGMRLRCDDMGSENDDMSEEDRLMLDRSPDELGSNDNDDDLGDSDSDEDLMA
ETTDGERIIY PWMKKHYAGVANGSYQPGMEPKRQRTAYTRHQILELEKEFHYNRYLT
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                                                                                                                                                                                                                                                                                       /db_xref="FLYBASE:FBan0001030"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(<46894. .>70354)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTASTGHMSGAVGGGAGVGSVGGGGAGGMTGHPHSMHPADMVSDYMAHHHNPHSHSHS
HTHSLJCHHHSNSAISGHQASAGGYSSNYANATPPSHPHSHPHAHPHQSLGYYVHHAP
EFISAGAVHSDPTNGYGPAANVPNTSNGGGGGGSGAVLGGGAVGGSANGYYGGYGGGY
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                                                                                                                                                                                                                 /product="CT1096"
                                                                                                                                                                                                                                                                                                                                                                                      /note="CG1030"
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from the published sequence for this transcript."
/db_xref="FLYBASE:FBan0002189"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Dfd gene product; Nucleotide sequence of the Celera sequence differs from the published sequence for this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="CG2189"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Dfd"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product-"CT7132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="3R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23761)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from the published sequence for this
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scklqaavgglgmypEggspplvDQmsghhmnaQmtlphhmghpQaqlgytdvgypDv
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Matches
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                                                                                    Local Similarity
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58.8%;
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                                                                                        Score 27; DB 3; Length 309357; Pred. No. 19;
                                                                         Mismatches
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Search completed: March 17, 2003, 11:24:06
Job time: 920.892 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

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25.6	26.4	27	20	28	28	Score
37.6	38.8	39.7	41.2	41.2	41.2	Query Match Length DB
533	688	3785	5 6	83	68	Length
24	19	23	20	19	18	DB
AAX19656 ABQ51034	AAV12903	ABL03968	AAX19657	AAV12904	AAV09396	IJ
Oligonucleotide SE Oligonucleotide fo	Chimeric repair ve Chimeric mutationa	Oligonucleotide us Drosophila melanog	Oligonucleotide SE	Chimeric mutationa	Chimeric repair ve	Description

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"RNA nucleotides"

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"DNA nucleotides"

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misc_feature

ALIGNMENTS

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FT /*tag= c	misc_feature	fT /note= "RNA nucleotides"	FT /*tag= b	misc_RNA		FT /*tag= a	misc_feature	FH Key Location/Qualifiers		OS Homo sapiens.	OS Synthetic.				KW Chimeric repair vector; CRV; treatment; genetic mutation; repair;		DE Chimeric repair vector (CRV) SC4.		DT 14-MAY-1998 (first entry)	XX	AC AAV09396;	XX	ID AAV09396 standard; DNA; 68 BP.	RESULT 1 AAV09396
													hybrid; ss.	her disease; emphysema;	etic mutation; repair;									

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RESULT 2
AAV12904
ID AAV1
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AC AAV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This chimeric repair vector (CRV) SC4 is used in comparative studies on CC the experimental use of a CRV SC1 designed to repair the mutation found CC in Sickle cell disease beta-globin and the beta-globin of a HSC. The CRV CC designed to repair the mutation contains a nucleic acid having at most CC one 3' end and one 5' end comprising a segment of unpaired bases (CC disposed. The unpaired bases separate the nucleic acid into a first CC strand and a second strand, comprising a first region and a second region comprising a first region and a second region comprising a first region and the first region having at least 15 nucleotides. Each nucleotide of the first region comprises at least 8 ribonucleotides which captured to a nucleotide of the second comparate the second region and the first region comprises at least 8 ribonucleotides which captured to 2'-deoxynucleotides, which ribonucleotides captured to at least 15 ribonucleotides captured to a tleast 15 ribonucleotides captured to a tleast 15 ribonucleotides captured to 2 repairing genetic mutations in cells for re-introducing into a patient comparation of a wild-type allele of a human gene. The CRVs can be used for treating diseases. They can be used for treating, sickle cell clience embrycems or hasmoshilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                  Chimeric mutational vector; alkaline phosphatase gene; gene repair; disease-related mutation; human; Gaucher's disease; sickle-cell anaemia; thalassemia; familial hypercholesterolaemia; emphysema; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric mutational vector
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                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               emphysema or haemophilia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0640517.
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                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kmiec EB,
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   /note= "binds to nucleotides 54 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                              SC4
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AAX19657;

AAX19657 standard;

DNA;

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02-JUN-1999

(first entry)

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RESULT 3
AAX19657
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                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                               thalassemia, familial hypercholesterolaemia, emphysema etc.). The chimeric mutation vectors are also used to inactivate specific genes, i.e. to generate transgenic ('knockout') animals or plants. They are used for biomedical research and for pharmaceutical production. Any eukaryotic gene of known sequence can be altered, by replacement, deletion or addition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide for altering a genomic sequence in eukaryotes - particularly for correcting disease-related mutation(s) and for production of transgenic animals and plants
                                                                                                                                                                                                                                                                                                                                                           Sequence 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-1997;
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                                                                                                                                                                       CCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGCGC 68
                                                                                                                      CCTGAGGAGAAGACTGCTTTTGCAGUCUUCUCCTCAGGAGUCAGGUGCGCGTTTTTCGCGC
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                           BP; 11 A; 19 C; 19 G; 13 T; 6 U; 0 other;
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64..68
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55..59
/*tag=
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30..39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "binds to nucleotides
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                                                                                                                                                                                                                                                                   Score 28; DB 19; Length 68 Pred. No. 0.57;
                                                                                                                                                                                                                                             Mismatches
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RESULT 4
ANAVS2984
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AC AAVY
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DT 04-1
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KW Chi
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Best Local S
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01-MAY-1996;
17-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                          The present invention describes double-stranded oligonucleotides (I) containing fragments of wild-type human alleles. (I) are used to repair disease associated mutations in human cells. (I) are preferably used to treat sickle cell aneemia or thalassemia (mutations in the beta-globin gene, including the promoter region), or Gaucher's disease (mutations in the glucocarebrosidase gene), in haematopoietic cells. (I) may also be used to treat familial hypercholesterolaemia (mutations in the lowdensity lipoprotein receptor gene), emphysema (the alpha 1-anti-trypsin gene), haemophilia (the factor VIII gene) or Christmas disease (the factor IX gene), in hepatocytic cells. (I) provides repair of small genetic mutations. The present sequence represents an oligonucleotide
                                      Chimeric oligonucleotide; specific alteration; target sequence; Intramolecular duplex stability; intermolecular duplex stability; intermolecular duplex stability; indicase degradation; chemical stability; bydrolysis resistance; degradation resisitance; A-type helix formation; stable conformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Double-stranded oligonucleotides with containing a human wild-type allele - useful for repairing mutations in human cells, particularly those causing sickle cell anaemia or thalassemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome; genetic lesion; haematopoietic stem cell; hepatocyte; RNase; human wild-type allele; mutation; sickle cell anaemia; thalassemia; Gauchar's disease; glucocerebrosidase gene; hypercholesterolaemia; emphysema; haemophilia; Christmas disease; ss.
                                                                                                    Oligonucleotide used in the course of the invention.
                                                                                                                             04-DEC-1998
                                                                                                                                                      AAV52984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide
                                                                                                                                                                            AAV52984 standard;
                                                                                                                                                                                                                                                                                                                                           Sequence 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cole-Strauss AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1997;
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                                                                                                                                                                                                                                                        CCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGCGC
                                                                                                                                                                                                                                                                                                                                                                   the present invention.
                                                                                                                                                                                                                                      CCTGAGGAGAAGACTGCTTTTGCAGUCUCCCTCAGGAGUCAGGUGCGCCTTTTCGCGC
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                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Column 61-62; 40pp; English.
                                                                                                                                                                                                                                                                                                                                           BP; 11 A; 19 C; 19 G;
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JEFFERSON THOMAS
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96US-0640517.
96US-0664487.
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                                                                                                                                                                             DNA;
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66.7%;
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                                      A-type helix formation; stable conformation;
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                                                                                                                                                                                                                                                                                                     Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                           13 T;
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0.57;
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RESULT 5
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                                                   pharmaceutical;
                                                                                      Drosophila
                                                                                                               26-MAR-2002
                                                                                                                                       ABL03968;
                                                                                                                                                             ABL03968 standard; cDNA; 3785
                                                                                                                                                                                                                                                                                                                                                                              Sequence 68 BP; 13 A;
                                                                                                                                                                                                                                                                                                                                                                                                      measurements.
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39; Conserv
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                                                                                                                                                                                                                             83
                                                                                                             (first entry)
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                                                  gene;
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invention provides chimeric oligonucleotides comprising a stem portion having one or more nucleotides selected from 2'-0-alkyl-ribonucleotides, 2'-allyl-ribonucleotides, 2'-halo-ribonucleotides, 2'-o-methoxyethyl-ribonucleotides, 2'-branching group-ribonucleotides, 2'-o-methoxyethyl-ribonucleotides, 2'-branching group-ribonucleotides, and one or more ribonucleotides or 2'-o-branching group-ribonucleotides, and one or more loop portions. The chimeric oligonucleotides may be used for introduction of specific alterations into target nucleic acid sequences located in living organisms. They have increased intramolecular and intermolecular ouplex stability, increased resistance to nuclease degradation and increased chemical stability, resistance to hydrolysis and degradation, as compared to known chimeric oligonucleotides. They have structures which induce intramolecular and intermolecular Artype helix formation. They have highly stable conformations, as measured by thermal melting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This oligonucleotide is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New chimeric oligo:nucleotide(s) - which are useful for causing specific alterations in target nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCCAACGAGGGATGCTCTACTATTTTTAGTAGAGCATCCCTCGTTGGAAGTGCGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCCAACCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTT
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                                                                                   melanogaster expressed polynucleotide SEQ
developmental biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 26..29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 19; Length 68
Pred. No. 1.3;
3; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 T; 0 other;
cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pentaethylene oxide
                                                                                   ID NO 6386
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AAV09395
ID AAV0
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AC AAV0
XX Chin
XX Chin
XX Chin
XX Chin
XX Synt
XX Synt
XX Homc
XX Homc
XX Ins.
FT mis.
FT mis.
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FT mis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                     misc_RNA
                                                                                                                                                                                               Chimeric repair vector; CRV; treatment; genetic mutation; sickle cell disease; beta-thalassemia; Gaucher disease; er hypercholesterolaemia; haemophilia; DNA/RNA hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
            misc_RNA
                                                 misc_feature
                                                                                                                                                                                                                                             Chimeric repair vector (CRV)
                                                                                                                                                                                                                                                                                                                                                                                   3541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                          misc_feature
                                                                                                                                                              Homo sapiens.
                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                               AAV09395;
                                                                                                                                                                                                                                                                                                                      AAV09395 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3785 BP; 876 A; 851 C; 982 G; 1076 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 6386; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75.
P-PSDB; ABB59865.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-191637P.
2000US-0614150.
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/note=
45..54
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40..44
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30..39
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                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           39.7%;
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                                                             "RNA
                          "DNA nucleotides'
                                                                                                  "DNA
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                                                                                                                                                                                                                                                                                                                       68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                  nucleotides"
                                                             nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                 6,
                                                                                                                                                                                                                                                 SC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23; Length 3785;
                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                          emphysema
                                                                                                                                                                                                                       repair;
                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Location/Qualifiers

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RESULT 7
AAV12903
ID AAV12903
XX
AC AAV1
XX
DT 17--
DT 17--
DK Chin
XX
CKW Chin
XX
KW Chin
KW Chin
KW Chin
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KW Chin
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SY
KW Chin
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SY
FH Key
                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                               This chimeric repair vector (CRV) SC3 is used in comparative studies on CC the experimental use of a CRV SC1 designed to repair the mutation found comparison of a MSC. The CRV designed to repair the mutation contains a nucleic acid having at most come 3' end and one 5' end comprising a segment of unpaired bases come 3' end and one 5' end comprising a segment of unpaired bases comed strand, comprising a first region and a second region respectively, each region having at least 15 nucleotides. Each nucleotide of the first region is Watson-Crick paired to a nucleotide Scond cregion and the first region comprises at least 8 ribonucleotides, which are Watson-Crick paired to 2'-deoxynucleotides, which ribonucleotides form at least one ribonucleotide segment of at least 3 ribonucleotides compairing genetic mutations in cells for refintroducing into a patient compairing diseases. They can be used for treating, sickle cell disease, beta-thalassemia, familial hypercholesterolaemia, Gaucher
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                            Chimeric mutational vector; alkaline phosphatase gene; gene repair; disease-related mutation; human; Gaucher's disease; sickle-cell ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric nucleic acid repair vectors - used for treating diseases such as sickle cell disease, beta-thalassemia, Gaucher disease, hyper:cholesterolaemia, emphysema or haemophilia
                               Synthetic.
                                                                                                                                            Chimeric mutational vector SC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                               thalassemia;
                                                                                                                                                                           17-JUN-1998
                                                                                                                                                                                                          AAV12903;
                                                                                                                                                                                                                                        AAV12903 standard; DNA; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 68 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cole-strauss A, Kmiec EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1996;
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                                                                                                                                                                                                                                                                                                                       CCTGAGGAGAAGACTGCTTTTGCAGUCUUCUCCTCAGGAGUCAGAUGCGCGTTTTCGCGC 68
                                                                                                                                                                                                                                                                                                                                                   CCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGCGC 68
                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           emphysema or haemophilia.
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                               familial hypercholesterolaemia;
                                                                                                                                                                         (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                              12 A; 18 C;
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55..68
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                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                              38.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "RNA nucleotides"
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                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                               Score 26.4; DE Pred. No. 2.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              18 G; 14 T; 6 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yoon
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                                                                                                                                                                                                                                                                                                                                                                                                              DB 18;
                                                                               emphysema; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0 other;
                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                               anaemia;
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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CC This sequence represents a nucleotide analogue of the invention, termed a chimeric mutational vector (CMV). This sequence is directed against the continuous cell, and comprise: (a) a first strand (S1) having at least 15 cc eukaryotic cell, and comprise: (a) a first strand (S1) having at least 15 cc nucleotides (nt); at least 3 nuclease-resistant ribo-type nt (nt') and at least 3 contiguous ribo-type nt, the same as, or additional to, the nt'; cc and (b) a second strand (S2) in which the nt are Watson-Crick (WC) paired to the nt in S1. The contiguous ribo-type nt in S1 are WC-paired to cc 2'-deoxyribo-type nt, and at least one ribo-type nt is other than a cc 2'-O-methyl substituted nt. nt' are 2'-Ax-nucleosides; 2'-Ax-nucleosides or 2'-AR-nucleotides; A = oxygen, fluoro, chloro or bromo; when A = 0, cc X = hydrogen or 1-6c alkyl and R = 1-6c alkyl; when A is halo then R and cells (e.g. those associated with Gaucher's disease-related mutation in human cells (e.g. those associated with Gaucher's disease, sickle-cell anaemia, thalassemia, familial hypercholesterolaemia, emphysema etc.). The collection mutation vectors are also used to inactivate specific genes, i.e. to generate transgenic ('knockout') animals or plants. They are also used for biomedical research and for pharmaceutical production. Any eukaryotic gene of known sequence can be altered, by replacement,
밁
                          S
                                                                                     Query Match
                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide for altering a genomic sequence in eukaryotes particularly for correcting disease-related mutation(s) and for production of transgenic animals and plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7.2; Fig 3; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYJE-) UNIV
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                                                                                                                     Sequence 68 BP; 12 A; 18 C; 18 G; 14 T; 6 U; 0 other;
                                                                        Loca1
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                              ဖ
                          CCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGCGC
CCTGAGGAGAAGACTGCTTTTGCAGUCUUCUCCTCAGGAGUCAGAUGCGCGTTTTCGCGC
                                                                        Similarity
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JEFFERSON THOMAS
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64 . 68
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30..39
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45..54
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                                                                       38.8%;
65.0%;
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                                                        Score 26.4; DB 19; Length Pred. No. 2.2; Indels
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                                                        0;
89
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AAX19656
ID AAX196
XX

AAX19656 standard; DNA;

83

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism

cell differentiation; ds

Oligonucleotide for detecting cytosine methylation

SEQ IJ

NO 37625

0;

12-JUL-2002

(first entry)

0;

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ABQ51034
ID ABQ5
XX ABQ5
AC ABQ5
XX 12-J
XX 12-J
XX Olig
XX Huma
KW Huma
KW Gast
KW SNP;
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 39
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01-MAY-1996;
17-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome; genetic lesion; haematopoletic stem cell; hepatocyte; RNase; human wild-type allele; mutation; sickle cell anaemia; thalassemia; Gaucher's disease; glucocerebrosidase gene; hypercholesterolaemia; emphysema; haemophilia; Christmas disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                              containing fragments of wild-type human alleles. (I) are used to repair disease associated mutations in human cells. (I) are preferably used to treat sickle cell anaemia or thalassemia (mutations in the beta-globin gene, including the promoter region), or Gaucher's disease (mutations in the glucocerebrosidase gene), in haematopoietic cells. (I) may also be used to treat familial hypercholesterolæemia (mutations in the low-density lipoprotein receptor gene), emphysema (the alpha 1-anti-trypsin gene), haemophilia (the factor VIII gene) or Christmas disease (the factor IX gene), in hepatocytic cells. (I) provides repair of small genetic mutations. The present sequence represents an oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Double-stranded oligonucleotides with containing a human wild-type allele - useful for repairing mutations in human cells, particularly those causing sickle cell anaemia or thalassemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO:95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cole-Strauss AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 68 BP; 12 A; 18 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes double-stranded oligonucleotides (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Column 59-60; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-243264/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYJE-) UNIV
                                                                                                                                        ABQ51034;
                                                                                                                                                                      ABQ51034 standard; DNA; 533 BP
                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                             CCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGCGC 68
                                                                                                                                                                                                                                                                                                                                                                                                      the present invention.
                                                                                                                                                                                                                                                CCTGAGGAGAAGACTGCTTTTGCAGUCUUCUCCTCAGGAGUCAGAUGCGCGCTTTTCGCGC 68
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0906265.
96US-0640517.
96US-0664487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0906265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kmiec
                                                                                                                                                                                                                                                                                                                        38.8%;
                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                        18 G; 14 T; 6 U; 0 other;
                                                                                                                                                                                                                                                                                                                        Score 26.4; D
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 10
ABQ51035/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-cpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the Clabel on the amplicon. From the ratio of labels hybridised to the two Cclasses of oligomers, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC of the central nervous, cardiovascular, gastrointestinal and respiratory cystems etc., particularly by detecting mutations or single nucleotide CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue CC methylation status of many C residues to be determined simultaneously. ABD13410-ABQ54121 represent genomic DNA sequences used to illustrate the CC method for determining the degree of cytosine methylation described in CC the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                             Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 533 BP; 89 A; 62 C; 208 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                    12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ51035 standard; DNA; 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 ACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGTCGCGGGATTTTTTTTTTTTTTTTTTTGTAGGAAGGTTGGAAGCGCGAGATTTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from chemically treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                     for detecting cytosine methylation SEQ ID NO 37626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                       ₿₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25.6;
Pred. No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
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ABL38127
ID ABL3
XX
AC ABL3
XX
DT 08-A
XX
Huma
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This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC genomic sample of DNA. The sample is treated chemically to convert CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two CC classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC systems etc., particularly by detecting mutations or single nucleotide CC types and for investigating cell differentiation of cell or tissue CC types and for investigating cell differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously.

CC abglatone of the invention.

CC method for determining the degree of cytosine methylation described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; 56pp + Sequence Listing; 56pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-SEP-2001;
                                         the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amplicons from chemically treated DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-371829/40.
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05-SEP-2000;
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2000DE-1044543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guetig
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Sequence 533 BP; 174 A; 208 C; 62 G; 89 T; 0 other;

Matches Query Match Best Local : 12 ACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGCTTTTCGCG 67 Local Similarity Conservative 37.6%; 55.4%; Score 25.6; Di Pred. No. 7.1; 6; Mismatches 6, DB 19; 24; Length 533; Indels 0 Gaps 0

B Qγ RESULT 11 533 ATGTCGCGGGATTTTTTTTTTTTTTTTTTTTTTTTGTAGGAAGGTTGGAAGCGCGAGATTTAGGG 478

ABL38127;

ABL38127 standard; cDNA;

08-APR-2002 (first entry)

Human colon tumour antigen polynucleotide SEQ ID NO:1716

Human; colon cancer; colon tumour antigen; cytostatic; vaccine; tumour metastatic antigen; diagnosis;

WO200196388-A2

20-DEC-2001

08-JUN-2001; 2001WO-US18557.

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RESULT 12
AAI99525/c
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Best Local :
                16-MAR-2000
17-MAR-2000
18-AFR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
30-JUN-2000
07-JUL-2000
                                                                                                              31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                  Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                      17-JAN-2001; 2001WO-US01356
                                                                                                                                                                                                                         WO200155173-A2
                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                            neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of cancer in a patient. (I) can be mutant species primers for nucleic acid hybridisation, for preparing can be used in the diagnosis of a colon tumour.
                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO 23.
                                                                                                                                                                                                                                                                                                                                                               07-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              AAI99525 standard; cDNA; 1280 BP.
                                                                                                                                                                                                                                                                                                                                                                                             AAI99525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 435 BP; 114 A; 98 C; 91 G; 130 T; 2 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated colon tumor polynucleotide differentially expressed in colon tumor or colon metastatic tumor and polypeptides encoded by them, useful for inhibiting development of cancer in patient -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 CTTCTGAACAACTTAGGAGAAACTTTTGATCTTCAGCTTGGTAGATTTAATTGCCCAGT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-2000; 2000US-210899P.
20-FEB-2001; 2001US-270216P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TBOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
              2000US-0179065
2000US-0180628
2000US-0184664
2000US-0186350
2000US-0189874
2000US-01990076
2000US-0199123
2000US-0205515
2000US-020467
2000US-0214886
2000US-0214886
2000US-0216135
2000US-0216647
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55.98;
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13-CCT-2000;
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21-SEP-2000
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18 - AUG - 2000;

22 - AUG - 2000;

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23 - AUG - 2000;

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01 - SEP - 2000;
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06-SEP-2000;
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11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
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2000US-0234997
2000US-0235488
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2000US-0235834
2000US-0235834
2000US-0235836
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2000US-0232397
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2000US-0232399
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2000US-0232401
2000US-0233401
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2000US-0229287
2000US-022934
2000US-022934
2000US-022934
2000US-022939
2000US-022959
2000US-0230437
2000US-0231442
2000US-0231243
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2000US-0239937
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2000US-0225270.
2000US-0225447.
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2000US-0217487.
2000US-0217496.
2000US-0218290.
2000US-0220963.
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2000US-0227182
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2000US-0224519.
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08 - NOV - 2000;
17 - NOV - 2000;
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01-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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17-NOV-20
17-NOV-20
     The invention relates to novel human polynucleotides (AAI99513-AAI99538) and the encoded proteins (AAM99915-AAM99934) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, line, or increasital. (h) immune disorders and addison's disease.
                                                                                                                                Claim 1; SEQ ID NO 23; 465pp + Sequence Listing; English.
                                                                                                                                                                      New nucleic acids and polypeptides, useful for treating, preventing or
                                                                                                                                                                                                      P-PSDB; AAM99927
                                                                                                                                                           ameliorating human disorders and diseases
                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                 2001-451924/48.
urogenital;
                                                                                                                                                                                                                                            Barash SC,
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2000US - 0241826.
2000US - 024617.
2000US - 0246474.
2000US - 0246475.
2000US - 0246476.
2000US - 0246476.
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                                                                                                                                                                                                                                                                                                                                                              2000US-0251856.
2000US-0251868.
                                                                                                                                                                                                                                                                                                  2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0256719.
 (b) immune disorders e.g. Addison's disease
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The invention comprises the amino acid and coding sequences of six human genset metabolic genes (GMG-7A, GMG-7B, GMG-8, GMG-9, GMG-10 and GMG-11). The GMG DNA and protein sequences of the invention are useful for treating or preventing metabolic-related disorders, such as: obesity;

impaired glucose tolerance; insulin resistance; Syndrome X; Type II diabetes; hyperlipidaemia; atherosclerosis; hypertension; and heart

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such a myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1280 BP; 345 A; 277 C; 257 G; 398 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genset metabolic gene (GMG-7A) cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL44063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL44063 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  impaired glucose tolerance; insulin resistance; Syndrome X; Type II diabetes; hyperlipidaemia; atherosclerosis; hypertens heart disease; cardiac insufficiency; coronary insufficiency; high blood pressure; insulin sensitiser;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                               WO200255694-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                       Treating or preventing a metabolic-related disease or disorder, e.g. obesity, impaired glucose tolerance, insulin resistance, Syndrome X, Type II diabetes, comprises administering Genset Metabolic Genes
                                                                                                                                                                                                                                                                             16-JAN-2001; 2001US-262235P.
                                                                                                                                                                                                                                                                                                            15-JAN-2002;
                                                                                            Disclosure; Page 113-116; 128pp; English.
                                                                                                                                                                               P-PSDB; AAO15420
                                                                                                                                                                                                                         Erickson MR, Bour BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CTTCCAACCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGT 60
                                                                                                                                                                                                2002-557821/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene; ss; gene therapy; genset metabolic gene; GMG-7A; GMG-7B;
GMG-9; GMG-10; GMG-11; metabolic-related disorder; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                             2002WO-IB01215
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 37..2169
                                                                                                                                                                                                                                                                                                                                                                                           /product= "Human GMG-7A protein"
                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA; 2257 BP
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Pred. No. 1
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                                                                                                                                                                                                                               Tanaka H;
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RESULT 14
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and treatment of cancer, leukaemmia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                  Claim 1; Page 4386-4387; 6221pp; English.
                                                                                                                                                                                                  useful in diagnosis and
                                                                                                                                                                                                      Nucleic acids encoding polypeptides with cytokine-like activities.
                                                                                                                                                                                                                                                          WPI; 2001-476283/51.
                                                                                                                                                                                                                                               P-PSDB; AAM79318
                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                27-APR-2000;
20-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2001; 2001WO-US04098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       .5-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine; peptide therapy; stem cell growth factor; haematopolesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK52451 standard; cDNA; 2454 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1849 CTTCTGAACAACTTAGGAGAAACTTTTGATCTTCAGCTTGGTAGATTTAATTGCCCAGT 1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK52451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases (e.g. cardiac insufficiency, coronary insufficiency or high blood pressure). The GMG DNA and protein sequences of the invention may also be used as insulin sensitisers - for improving insulin sensitivity in persons with non-insulin dependent diabetes mellitus. The present cDNA sequence encodes the human GMG-7A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2257 BP; 728 A; 522 C; 482 G; 525 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CTTCCAACCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                               Liu C, Drmanac RT, Asundi V, Zhou
Wang D, Wang J, Zhang J, Ren F, C
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                      ; 2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-063936.
2000US-063326.
2000US-0693325.
2000US-0728422.
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55.98;
                                                                                                                                                                                                gene therapy -
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Pred. No. 12;
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AAK52452
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                                                                                                                                                                                                                                                                                  19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
                                                                                                               Claim 1; Page 4387-4388; 6221pp; English.
                                                                                                                                       useful in diagnosis and
                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                WPI; 2001-476283/51.
                                                                                                                                                                                                Zhao QA, Wang D, Wang J, Zi
Xue AJ, Yang Y, Wejhrman T,
                                                                                                                                                                                                                 Tang YT,
Zhao QA,
                                                                                                                                                                       P-PSDB; AAM79319
                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                 30-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polynucleotide SEQ ID NO 1981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2175 CTTCTGAACAACTTAGGAGAAACTTTTGATCTTCAGCTTGGTAGATTTAATTGCCCAGT 2233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK52452 standard; cDNA; 2454 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2454 BP; 782 A; 574 C; 532 G; 563 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CTTCCAACCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                             2000US-0663561.
2000US-0693325.
2000US-0728422.
                                                                                                                                                                                                                                                                                           2000US-0598075.
2000US-0620325.
2000US-0654936.
                                                                                                                                                                                                                                                                                                                          2000US-0496914.
2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                   37.4%;
                                                                                                                                       gene
                                                                                                                                     therapy
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                                                                                                                                                                                               Goodrich R;
                                                                                                                                                                                                       Asundi V, Zhou P,
lang J, Ren F, Chen
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Pred. No. 12;
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                                                                                                                                                                                                        R Xu C,
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity and may be useful in the diagnosis and/or treatment of cancer lankagemia across a subject of the content of cancer lankagemia across a subject of the content of cancer lankagemia across a subject of the content of cancer lankagemia across a subject of the content of cancer lankagemia across a subject of the content of cancer lankagemia across a subject of the content of cancer lankagemia across a cancer lankagemia across a content of cancer lankagemia across a content of cancer lankagemia across a content of cancer lankagemia across a cancer lankagemia across a content of cancer lankagemia across a content of cancer lankagemia across a cancer lankag

treatment of cancer, leukaemia, nervous system disorders, arthritis and

CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 CC (AAM80020) are omitted as the relevant pages from the sequence listing CC were missing at the time of publication.

XX Sequence 2454 BP; 782 A; 574 C; 532 G; 563 T; 3 other; SQ Sequence 2454 BP; 782 A; 574 C; 532 G; 563 T; 3 other;

Query Match
Best Local Similarity 55.9%; pred. No. 12;
Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

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Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Matches 33; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Matches 3

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Title:
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Sequence:
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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25.8	25.8	25.8	25.8	27	27	Score
37.9	37.9	37.9	37.9	39.7	39.7	Query Match Length DB ID
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вQ937919	вQ946406	BI733738	в1739136	CNS0034I	BG188346	ID
BQ937919 AGENCOURT	BQ946406 AGENCOURT	BI733738 603352352	BI739136 603361404	AL063844 Drosophil	BG188346 RST7364 A	Description

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ALIGNMENTS

FEATURES	JOURNAL MEDLINE COMMENT	TITLE	REFERENCE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BG188346 LOCUS DEFINITION
Athersys, inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scainGathersys.com High quality sequence stop: 440. Location/Qualifiers	activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001) 21227151 Contact: Scott J. Cain	Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M. Creation of genome-wide protein expression libraries using random	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 818) Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,		BG188346 818 bp mRNA linear EST 21-APR-2001 RST7364 Athersys RAGE Library Homo saplens cDNA, mRNA sequence.

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ORIGIN
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                                                                         Local
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
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TAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCG 65
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster
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                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                               /clone_lib="RPCI-98"
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/db_xref="taxon:9606"
/clome_lib="Athersys RAGE Library"
/cell_line="HT1080"
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58.8%;
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National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                              BI733738 747 bp mRNA linear EST 20-5EF-20 603352352F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5359908 5',
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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BI733738
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Tissue Procurement: The Cepko Laboratory
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: WGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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//tissue_type="retina"
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/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Total continuation of the continuation of th
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                                                                                                                                                           Euteleostomi;
Murinae; Mus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; I
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; I
1 (bases 1 to 899)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11915 row: g column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 614.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM13993 row: 1 column: 17
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5', mRNA sequence.
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Tissue Procurement: The Cepko Laboratory
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National Institutes of Health, Mammallan Gene Collection (MGC)
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/db_xref="taxon:10000"
/clone="IMAGE:5359908"
/clone_lib='NII_MCC_94"
/tlssue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note
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/Clone_lib="NIH_MCC_94"
/tissue_type="retina"
/lab_host="Ph10B (phage-resistant)"
/lab_host="Ph10B (phage-resistant)"
/late="Organ: eye: Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT prime
Average insert size 3.3 kb. Library enriched for
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/clone="IMAGE:6467512"
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Pred. No. 47;
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Mus musculus cDNA clone IMAGE:6467512
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20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammalian Gene Collection (MGC)
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BG262012.1 GI:12771828
                                BG26201
                                                          mRNA sequence.
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Mammalia; Eutheria; Rodentia;
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/db_xref="taxo":1090"
/clone="mMAGE:6468857"
/clone="lib="NIH_MGC_94"
/tlssue_type="retina"
/lab_host="bH10B (phage-resistant)"
/lab_host="bH10B (phage-
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Note: this is a NIH_MGC Library."
a 208 c 231 g 207 t 5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25.8;
Pred. No. 50;
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Pred. No. 50;
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                                                                                           IMAGE: 4481291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTITCTGCTACGTAGGTTGGAAGGCCAC 443
                                                                                                                                                                                                                                                                          house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; l

1 (bases 1 to 961)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston

Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Manuel 1 (bases 1 to 943)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMI0318 row: a column: 16
                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG342737
BG342737.1 GI:13149175
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: The Cepko Laboratory
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house mouse
                  High quality sequence stop: 653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
a 230 c 256 g 188 t
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Pred. No. 51;
7; Mismatches
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Sciurognathi; Muridae; Murinae; Mus.
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LOCUS
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TITLE
Matches
                 Query Match
Best Local :
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                     Plate: LLAM10376 row: 1 column: High quality sequence stop: 735.
                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10376 row: 1 column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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             Similarity
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Conservative
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                                                           /clone_lib="NII_FVC_...
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 218 c 254 g 201 t
                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4504476"
/clone_lib="NIH_MGC_94"
                                                                                                                                                                                                                                                                                                                            1. .1101
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/clone="IMAGE:4481943"
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                 37.9%;
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                 Pred.
                                   Score 25.8;
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Pred. No. 51;
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Mismatches
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                                   Length 1101;
Indels
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E:4504476 5',
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Gaps
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30 ACUUUCUGCUACGTAGGUUGGAAGGGCGC

무

76 ACTITCIGCTACGTAGGTTGGAAGGCCAC 48

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COMMENT
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AUTHORS
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305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                         Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondal 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrharcoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                            AU096979
AU096979 Rice green shoot Oryza sativa (japonica cultivar-group)
CDNA clone S16784, mRNA sequence.
                                                                                                                                                                                               Rice cDNA from green shoot (2000) Unpublished (2000)
                                                                                                                                                                                                                                          Sasaki,T.
                                                                                                                                                                                                                                                                                                                                                                                          AU096979.1 GI:8859661
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National Institute of Agrobiological Resources
Rice Genome_Research Program, Kannondal 2-1-2, Tsukuba, Ibaraki
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                            (bases 1 to 297
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81-298-38-7468
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                                                                                                                                                                                                                                      and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"
79 c 68 g 57 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
Cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="$16022"
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8 ACCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G. International Triticeae EST Cooperative (ITEC): Production of
                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                         http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  Key Lab. of Crop Germplasm & Biotechnology
Inst. of Crop Germplasm Resources
Beijing 100081 pR CHINA
Tel: 86 1 62186623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                       International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNW02EL010 ITEC CNW Wheat Powdery Millow Resistant Library Triticum cDNA clone CNW02EL010, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 jizeng@mimi.cnc.ac.cn
                                                                                                                   /note="Vector: Lambda TriplEx; Site_1: SfiI; Primer used:
5'-TCCGAGATCTGGACGAGC-3' 500 bp average insert size."
a 81 c 87 g 48 t
                                                                                                                                                                                     strain"
                                                                                                                                                                                       /dev_stage="seedling, challenged with powdery mildew
                                                                                                                                                                                                                                       Library"
                                                                                                                                                                                                                                             /clone_lib="ITEC CNW Wheat Powdery Mildew Resistant
                                                                                                                                                                                                                                                               /organism="Triticum aestivum"
/cultivar="Powdery Mildew Resistant line"
/db_xref="taxon:4565"
/clone="CNW02EL010"
                                                                                                                                                                                                                   /tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"
84 c 72 g 56 t
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1. .297
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/db_xref="taxon:39947"
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                                                        37.6%;
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                                   5; Mismatches 14; Indels
                                                         Score 25.6; DB 10;
Pred. No. 41;
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Pred. No. 41;
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AU070730 Rice cDNA from young root Oryza sativa (japonica cultivar group) cDNA clone R10161_2A, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryza.
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AU057142 Oryza sativa mature leaf Nipponbare Oryza sativa (japonica cultivar-group) cDNA clone S21188_1A, mRNA sequence.
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                                                                                                         Unpublished (1999)
Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                              AU057142.1 GI:4716026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                   305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
                                                                   Rice Genome Research Program, Kannondai 2-1-2, Tsukuba,
                                                                                    National Institute of Agrobiological Resources
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                 Yamamoto, K. and Sasaki, T.
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81-298-38-7441
81-298-38-7468
                                                                                                                                              cDNA from mature leaf
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98 c 96 g 97
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/db_xref="taxon:39947"
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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AU162789 Rice mature leaf Oryza sativa (japonica cultivar-group)
cDNA clone S21904, mRNA sequence.
AU162789
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                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Takuji Sasaki
National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki, T. and Yamamoto, K.
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
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/clone="S21188_1A"
/clone=lib="Oryza sativa mature leaf Nipponbare"
/tissue_type="mature leaf"
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/tissue_type="mature leaf"
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ALIGNMENTS

REFERENCE AUTHORS		MSIN	SEGMENT	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	MMHIF1AS04	RESULT 1
<pre>1 (bases 1 to 85) Luo,G., Gu,Y.Z., Jain,S., Chan,W.K., Carr,K.M., Hogenesch,J.B. and Bradfield,C.A.</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.	Mus musculus	4 of 15		AF004144.1 GI:2197137	AF004144	Mus musculus hypoxia-inducible factor 1 alpha (Hilla) gene, exon 4.	MMHIF1AS04 85 bp DNA linear KOD 25 NOV 1997		

Pred. No.

is the number of results predicted by chance to

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         noHIFIAU3 538 bp DNA linear PRI 26-OCT-1998 Homo sapiens hypoxia-inducible factor 1 alpha subunit (HIF1A) gene, exons 3 and 4.
                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                       evolutionary conservation
Genomics 52 (2), 159-165 (1998)
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The human hypoxia-inducible factor lalpha gene: HIFlA structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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/number=4
                                                          /gene="HIF1A"
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/db_xref="taxon:9606"
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/db_xref="taxon:10090"
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Sequence 3 from Patent W00212326.
AX451938
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Mechanism of conditional regulation of the hypoxia-inducible
factor-1 by the von hippel-lindau tumor suppressor protein
Patent: WO 0212326-A 3 14-FEB-2002;
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CLVLICEPI PHESNI ELPLDSKTFLSRISLDMKFSYCDERITELMGYEPELLGRSIY
EYYHALDSDHLTKTHHDMFTKGQVTTGGYRMLAKRGGYVWVETQATVIYNTKNSQPQC
IVCVNYVYSGI IQHDLITSLQOTECVLKPVESSDMKMTOLFTKYESEDYSSLFDKLKK
EPDALTILAPAAGDT I ISLDFGSNDTETDDQOLEEVPLYNDWLPSPNEKLQNTNLAM
SPLPTAETFK PLRSSADPALNQEVALKLEPNESSLELSFTWAPOJODQTPSPSDGSTRQ
SSPERNSPSEYCFYVDSDMVNEFKLELVELFAEDTEAKNPFSTDDTDLDLEMLAPYI
PMDDDFQLRSFOLTSPLESSSASPESASPCSTVVVFQQTQIQEPTANATTTATDEL
KTVTKDRMEDIKILIAPSPSHTHKETTSATSSPYRDTQSRTASFNRAGKGVIEQTEK
SHPRSPNVLSVALSQRTTVPEEELNFKILALQNAQRKKKMEHDGSLFQAGGTGTLLQQ
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DCEVNAPIQGSRNLLQGEELLRALDQVN"
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PLPHNVSSHLDKASYMRLTISYLRVRKLLDAGDLDIEDDMKAQMNCFYLKALDGFVMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAD37798.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sun, B., Zhao, H.R.,
Direct Submission
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1 (bases 1 to 2509)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKRKMEHDGSLFQAVGIGTLLQQ
                 PMDDDFQLRSFDQLSPLESSSASPESASPQSTVTVFQQTQIQEPTANATTTTATTDEL
KTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYRDTQSRTASPNRAGKGVIEQTEK
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                                                                                                                                                                                                                                                                      /gene-"HIF1A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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HIFIa sequence in the Quechua, a high altitude population
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Homo sapiens hypoxia-inducible factor l alpha (HIFIA) gene,
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/codon_start-1
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GEDALTLAPAAGDTIISLDFGSNDTETDDQQLEEVPLYNDVNLDSPHEKLQNINLAM
SPLPTAETPKPLRSSADPALNQEVALKLEPHPESLELSFTMPQIODTPSPSDGSTRQ
SSPENNSPSEYCFYUDSDMVNEFKLELVEKLFAEDTBAKNPFSTQDTDLLEMLAPYI
PMDDDFQLRSFDQLSFDLSFLESSSAPQSTVTVFQQTQ10gbTANATTTTATTDEL
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SHPRSPNLSVALSQRTVPEEELNPKILALQNAQRKRKMEHDGSLFQAVGIGTTLLQQ
PDDHAATTSLSMKRVKGCKSSEQNGMEGQKTIILIPSDLACRLLGQSNDESGLPQLTSY
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                 DCEVNAPIQGSRNLLQGEELLRALDQVN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="14q21-q24"
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/chromosome="14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="HIF1-alpha"
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DCEVNAPIQGSRNLLGGEELLRALDQVN*
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Query Match

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Score 23.4;

DB 9;

Length 2522;

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Sequence 2 from Patent WO0162965.
AX230580
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Location/Qualifiers
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                                                                                                                                                                                         Submitted (18-NOV-1999) Zoology, University of British Columbia, 6270 University Blvd., Vancouver, BC V6T 1Z4, Canada
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/db_xref="taxon:9606"
528 c 513 g 64
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/gene="HIF1A"
/note="HIF1-alpha"
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                                                                                              /map="14g21-g24"
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                                                                                                            /chromosome="14
                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                               /note="HIF1-alpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                              /codon_start=1
                                                                                                                                /gene="HIF1A"
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Submitted (27-FEB-1998) T. Kietzmann, Inst.
Cell Biol., Georg-August-Univ. Goettingen, F
                                                                                                                                                                                                                                                                                                                                                               D-37073 Goettingen, FRG
Revised by [3]
3 (bases 1 to 2711)
                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (18-NOV-1995) T. Kietzmann, Inst. Of Biochem. #
Cell Biol., Georg-August-Univ. Goettingen, Humboldtallee
                                                                                                                                                                                                                   D-37073 Goettingen, FRG
On Mar 4, 1998 this sequence version replaced gi:2632130.
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                                                                                                                                                                                                                                                                                                                                                   Kietzmann,T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kietzmann,T
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2711 bp mRNA linear
norvegicus mRNA for hypoxia-inducible factor 1.
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CYYHYVYSGIIQHDLIFSLQQTECVLKPVESSDMKMTQLFTKVESEDTSSLFDKLKK
EPDALTLLAPAAGDTIISLDFGSNDTETDDQQLEEVYLNDVHLDSPMEKLQNINLAN
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124. .2601
                                                                                                            /organism-"Rattus norvegicus"
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/db_xref-"taxon:10116"
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KTVTKDRMEDIKILIASPSPTHIKETTSATSSPYRDTQSRTASPNRAGKGVIEQTEK
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/codon_start=]
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PLPHAVSSHLDKASVMRLTISYLRVRKLLDAGDLDIEDDMKAQMNCFYLKALDGFVMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 3551)
Tanaka, S. and Sugimachi, K.
Direct Submission
Submitted (20-ocr-2001) Shinji Tanaka, Kyushu University, Graduate School of Medical Sciences, Department of Surgery and Science; 3-1-1 Maidashi, Fukuoka, Fukuoka 812-8582, Japan (E-mail:shinjittsurg2.med.kyushu-u.ac.jp, Tel:81-92-642-5466,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanaka, S. and Sugimachi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax:81-92-642-5482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB073325.1 GI:16326343
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AB073325
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GDRAPTMSLSWRRVKGYISSEODGMEOKTIFLIPSDLACRLLGQSMDESGLPQLTSYD
CEVNAPIQGSRNLLQGEELLRALDQVN"
1 613 c 623 g 677 t
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IVCVNYVSGIIQHDLIFSLQQTESVLKPVESSDMKMTQLFTKVESEDYSCLFOKKK
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MDDDFQLRSFDQLSPLESNSBSPSTGVFQENTTAKASATSGTHSRTASPDRAGKRVIEKTDX
KAVTKONIEDIKILASPPSTQVPQEMTTAKASATSGTHSRTASPDRAGKRVIEKTDX
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/db_xref="GI:2632131"
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                                                                                                                                                                           /note="HIF-1 alpha variant"
                                                                                                                                                                                                        /gene="HIF1A"
                                                                                                                                                                                                                                                       /gene="HIF1A"
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                       'tissue_type="liver"
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Pred. No. 0.
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U22431.1
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Genetics, The Johns Hopkins University Sc.
Wolfe St., Baltimore, MD 21287-3914, USA
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Hypoxia-inducible factor 1 is a basic helix-loop-helix-PAS
heterodimer regulated by cellular O2 tension
Proc. Natl. Acad. Sci. U.S.A. 92 (12), 5510-5514 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang, G.L., Jiang, B.-H., Rue, E.A. and Semenza, G.L. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CLYLICEPIPHPSNIEIPLDSKTFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIY
EXYHALDSDHLTKTHHOMFTKGÇVTTGQYRMLAKRGGYYWVETÇATVIYNTKNSQPQC
IYCVNYVYSGIIQHDLIFSLQQTECVLKPVESSDMKMTQLFTKVESEDTSSLFDKKKK
EPDALTILAPAAGDTIISIDFGSNDTETDDQQLEEVPLYNDVMLPSPNEKLQNINLAM
SPLPTAETPKPLRSSADPALNQEVALKLEPNPESLELSFTMPQIQDTPSPSDGSTRQ
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CLVLICEPIPHPSNIELPLDSKTFLSRHSLDMKFSYCDERITTELMGYEPEELLCRSIY
EXYHALDSDHLTKTHHDMFTKGQVTTGQYRMLAKRGGYVWVETQATVIYNTKNSOPQC
IVCVNYVSGIIQHDLIFSLQQTECVLKPVESSDMKMTQLFTKVESEDTSSLFDKLKK
EPDALTLAPAAGDTIISLDFGSNDTETDDQQLEEVPLYNVVESPPNSKLQNINLAM
SPLPTAETPKPLRSSADPALNQEVALKLEPNEPSLELSFTMPQIQDGYPSPDGSTRG
SSPEPNSPSEYCFYVDSDMVNEFKLELYEKLFAEDTEAKNPFSTQDTDLDLEMLAPYI
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/protein_id="AAC50152.1"
/db_xref="GI:881346"
/translation="MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQL
PLPHNVSSHLDKASYMRLTISYLRVRKLLDAGDLDIEDDMKAQMNCFYLKALDGFYMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PMDDDFQLRSFDQLSPLESSSASPESASPQSTVTVFQQTQIQEPTANATTTTATTDEL
KTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYRDTQSRTASPNRAGKGVIEQTEK
                                                                                                                      LTDDGDMIYISDNVNKYMGLTQFELTGHSVFDFTHPCDHEEMREMLTHRNGLVKKGKE
QNTQRSFFLRMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYDTNSNQPQCGYKKPPMT
                                                                                                                                                                                                                                                                                                                                                                                        /gene="HIF-1 alpha" 29. .2509
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                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                 /standard_name="hypoxie-inducible factor 1,
/note="basic helix-loop-helix transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _line="Hep3B"
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Pred. No. 0.
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SOURCE

KEYWORDS VERSION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-APR-1998) Departments of Physiology and Pharmacology, Medical College of Wisconsin, 8701 Watertown Plank Road, Milwaukee, WI 53226, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 3718) Equation 1. It is and Cowley AW, J.R. 20u, A.P., Yang, Z.Z., Li, P.L. and Cowley AW, J.R. Oxygen-dependent expression of hypoxia-inducible factor-lalpha in renal medullary cells of rats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Physiol. Genomics (Online) 6 (3), 159-168 (2001)
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KTYTKDMEDLKILASPSPTHIHKETTSATSPSTDTGSTTASPNRAGKGVIEQTEK
SHPRSPNLLSVALSQRTYPEEELNFKILALQNAQRKRKMEHDGSLFQAVGIGTILQQ
PDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLACRLLGQSMDESGLPQLTSY
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KEPDALTLLAPAAGDTIISLDFGSDDTETEDQQLEDVPLYNDVMFPSSNEKLNINLAM
SPLPASETPKPLRSSADPALNQEVALKLESSPESLGLSFTMPQIQDQPASPSDGSTRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
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                                                                                                                                                      YEYYHALDSDHLTKTHHDMFTKGQVTTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="transcription factor; RH1F-1"
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/dev_stage="adult"
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Wenger, R.H., Rolfs, A., Marti, H.H., Guenet, J.L. and Gassmann, M. Nucleotide sequence, chromosomal assignment and mRNA expression of mouse hypoxia-inductble factor-1 alpha Biochem. Blophys. Res. Commun. 223 (1), 54-59 (1996)
                                                                     Zuerich, SWITZEKLAND
Revised by author 16-JUL-96
2 (bases 1 to 3746)
2 (bases 1 to 3746) Mart
                                                                                                                Direct Submission
Submitted (07-FEB-1996) R.H. Wenger, Institute of Physiology, University of Zuerich-Irchel, Winterthurerstrasse 190, CH-8057 Zuerich, SWITZERLAND
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3746)
                                                                                                                                                                                                   Wenger, R.H.
                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                           X95580.1 GI:1430864
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M.musculus mRNA for hypoxia-inducible factor I alpha.
X95580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for examining ischemic conditions
Patent: WO 0188188-A 759 22-NOV-2001;
School Juridical Berson Wilhon University (JP)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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740 c 740 g 1
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YTXDNIEDIKILLASPPSTQVPQEMTTAKASAYSGTHSRTASPDRAGKRVIEKTDKAH
PRSLNLSVTLNQRNTVPEEELNPKTIALQNAQRKRKMEHDGSLFQAAGIGTLLQQPGD
RAPTMSLSWKRVKGYISSEQDGMEQKTIFLIPSDLACRLLGQSMDESGLPQLTSYDCE
VNAPIQGSRNLLQGEELLRALDQVN"
133 c 762 g 1098 t
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/db_xref="SWISS-PROT:061221"
/db_xref="SWISS-PROT:061221"
/db_xref="SWISS-PROT:061221"
/translation="MSSERKEKSRDAARSRRSKESEVEYELAHOLPHNVSSHLDKASVWRLTISYLRVKKLLDAGGLDSEDEWKAOMDCFYLKALDGEVWLTDDGDWYISD NVNKYMCLTOFELAGHSVEDFTHECDHEEMREMLTHRNGPVRKGKELNTQRSFFLRMKGNWKYMCLTOFELAGHSVEDFTHECDHEEMREMLTHRNGPVRKGKELNTQRSFFLRMKGNIEIPLDSKTFLSGRTMNIKSATMKVLHCTGHIHWSINOPQCKKRPRWTCLVLICEPIPHPKSNIEIPLDSKTFLSGRSHSLDMKFSYCDERITELMGYEPEELLGRSIYEYYHALDSDHLTKTHHDMETKGOVTTGOVRANLARRGGYVWVETOATVIYMTKNSOPQCIVCVNYVYSGIIQHDLIFSSLOQTESYLKFVESSDMKMTQLFKFVSEDTSCLFFNKLKEPDALTLLAPAAGTILLAFATDSCLFSTFKPLRSGDTILLAFAAGAGTILLAFATDSCLFSTFKDKKBDLFSSTFKPLRSSADDALNACHSSPESGCLSFTMPQIODQPASPSDGSTRQSSPENSFPSDGSTGCASPTOLARPATTTAATTDESKTFTKONKBDLKILIASPSCHOLSTTAAATTDESKTFTKONKBDLKILIASPSCHOLSTTAAATTDESKTFTKONKBDLKILIASPSCHOLSTTAAATTDESKTFTKONKBDLKILIASPSCHOLSTTAAATTDESKTFTKONKBDLKILIASPSCHOLSTTAAATTDESKTFTKONKBDLKILIASPSCHOLSTTAKAATSCHOLSTTAAATTDESKTFTKONKBDLKILIASPSCHOLSTTAKAATSCHOLSTTAAATTDESKTFTKONKBDLKILIAAPSTOOLSTTAKASAXSCTHSRTAASBDRAGKRVLEOTDKAHPRSLNLSATLNQR
                                                                                                                                                                        GEELLRALDQVN'
                                                                                                                                                                              GFISSEQNGTEQKTIILIPSDLACRLLGQSMDVSGLPQLTSYDCEVNAPIQGSRNLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypoxia-inducible factor one alpha"
/protein_id="CAA64833.1"
/b_xref="GI:4379202"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="HIF-lalpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                            740 c
                                    93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "HIF-lalpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     line="Hepalc1c7"
              0;
                                    Score 23.4; DB 10;
Pred. No. 0.38;
                                                                                                                                         740 g 1142 t
           Mismatches
        Indels
                                                          Length 3746;
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Gaps
0
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seg length: 0 seg length: 2000000000
                         IDENTITY_NUC Gapext 1.0
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25
SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA199.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

07-AUG-2000; 2000US-223480P

07-AUG-2001; 2001WO-IB01775

14-FEB-2002.

WO200212326-A2.

/product= "HIF-1"

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7545 7545 7545 21469	3625 3625 3708 4172 4172	2987 2987 3183 3183 3193	1174 1174 1707 2158 2159 2280	439 477 477 480 813	367 589 1070 1070	3927 3933 4162 10355 27884
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ABA09525 AAK53401 AAK53402 AAK89568	AAH46859 AAH78738 ABA05449 ABV23038 ABV28874	AAI93889 AAH16184 AAS71919 AAS84255 AAS78605	AAF15982 AAH33713 AAS81186 AAS78604 AAS71921 AAH18074	ABV13952 ABV35061 ABV35061 ABV43908 ABV4783 AAA44916 AAH06353	AAH93977 ABK62425 AAC75526 ABN77923 AAC78871	AAS61690 AAX58980 AAS85058 AAS14156 AAK77781
secreted polynucle polynucle digestive	/thre 1 ser ripti te ex	Human stomach cance Human stomach cance Human cDNA sequenc DNA encoding novel DNA encoding novel DNA encoding novel		Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human secreted exp Human cDNA clone (equence di ORFX ORF1 ORF2870 c	Lung small cell ca Human transcriptio DNA encoding novel pSMART CMV-HIF DNA Human immune/haema

ALIGNMENTS

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RESULT 1
ABK11552
                                                                                                                                                                                 Human; ss; gene; HIF-1; hypoxia-inducible factor-1; transactivation domain; N-TAD; C-TAD; ischaemia; brain infarction; circulatory disorder; cancer; hypertension; demyelinating disorder; angiogenesis; sarcoidosis; hepatitis-caused inflammation; chronic ulceration; neovascularisation; arterial hypervascularisation; bullous skin disease; vasculitis; dermatomyositis; polymyositis; rheumatoid arthritis.
                                                                                                                                                                                                                                                                               Human cDNA encoding hypoxia-inducible factor-1 alpha, HIF-1.
                                                                                                                                                                                                                                                                                                            05-JUN-2002 (first entry)
                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                              ABK11552 standard; cDNA; 2481
                                                                                                                      Location/Qualifiers
1..2481
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RESULT 2
ABL91695
Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulates N-TAD function and antagonists, agonists, modulators and HIF-1 peptide fragments useful for modulating HIF-1 function or the function of proteins that interact with it. The isolated polypeptides and their fragments with altered residues are useful in methods for treating diseases. The disease is an ischaemic condition, e.g. brain infarction, heart infarction or circulatory disorder. The disease may also be cancer, hypertension, demyelinating disorders, diffuse proliferative plomerulonephritis, toxoplasmosis caused retinochorioiditis, HIV (human immunodeficiency virus) caused Tat anglogenesis, HIV-caused Kaposi's sarcoma, hepatitis-caused inflammation, hepatitis-caused anglogenesis, sarcoma, hepatitis-caused inflammation, hepatitis-caused anglogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor-1 (HIF-1) with alterations of the transactivation domain (N-TAD of TAD). Also included are nucleic acids encoding the altered proteins, a vector comprising the nucleic acid, a host cell transformed with the vector, methods for producing the protein or its functional fragment or an isolated degradation box, a method of screening for an agent that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptides comprising hypoxia-inducible factor-1 with alterations of the transactivation domain, useful treating ischaemic conditions, e.g. brain infarction, heart infarction or circulatory disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chronic ulceration, proliferative retinopathy, retina haemangioblastomas, neovascularisation, arterial hypervascularisation, sarcoidosis, bullous skin disease, vasculitis with angiogenesis, dermatomyositis with angiogenesis, dermatomyositis with surfunction arthritis, juvenile osteoarthritis, polyarthritis, aneurysm or atheroma. The present sequence encodes HIF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 73-76; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAU77602
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                                                                                                                                                                                                                                       Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a polypeptide comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ASPE-) ASPERA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2481 BP; 829 A; 512 C; 500 G; 640 T; 0 other;
                                                                                                                                                             DE10100586-C1
                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                 28-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL91695 standard; DNA; 2481
                                                                             09-JAN-2001; 2001DE-1000586
                                                                                                                                                                                                 Homo sapiens
(RIBO-) RIBOPHARMA AG
                                     09-JAN-2001; 2001DE-1000586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               412 CCATGTGACCATGAGGAAATGAGAG 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.6%;
96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23.4; DB 24; Length 2481;
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                                                                                                                                                                                                                                                                                                                           38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               de comprising hypoxia-inducible the transactivation domain (N-TAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS14154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  terminal bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting gene expression in cells, useful for e.g. treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-270454/32.
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Screening a genetic element involved in a cellular process, comprises comparing gene expressions in a cell, and a second cell that has altered levels of genes used in the process, and detecting an element with varied expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Differential expression; polymorphism; biological pathway; IRES; GFP; ss; internal ribosome entry site; green fluorescent protein; HIF-1 alpha; hypoxia inducible factor 1 alpha; hypoxia regulated gene; macrophage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human HIF-1 alpha DNA used in identification of hypoxia regulated genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2481 BP; 829 A; 512 C; 500 G; 640 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS14154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS14154 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200162965-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2001
                                                                                                                                                                            Kingsman AJ;
                                                                                                                                                                                                                                                                                                                                                   22-FEB-2001; 2001WO-GB00758
                                                                                                                                                                                                                                                                                                                                                                                                 30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412
                                                                                                                                                                                                                         (OXFO-) OXFORD
                                                                                                                                                                                                                                                                            28-JUL-2000;
                                                                                                                                                                                                                                                                                                   22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                              2001-589807/66.
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                                                                                                                                                                                                                                                                          2000GB-0004197
2000GB-0018679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                              BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.6%;
96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complementary oligoRNA having unpaired
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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    whose expression differs, by comparing expression under different environmental conditions. The method is useful for identifying mutations and polymorphisms that affect the biological response to a particular cellular process. The method also allows the molecular dissection of biological pathways by altering a particular pathway under study. By introducing a heterologous nucleic acid into a cell population, the level of a particular molecule can be influenced, allowing a pathway to be dissected into its precise molecular components. The main use of the method is to compare gene expression in cells from a diseased patient of the from a normal patient. This sequence represents a human hypoxia inducible factor 1 alpha (HIF-1 alpha) which is inserted into an Adapt tree-GFF plasmid for use in identification of hypoxia-regulated genes in
                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to differential expression screening to identify a genetic element involved in a cellular process. The method involves comparing gene expressions in two cells, where one cell has altered levels of a biological molecule, and identifying the genetic element
           Regulation of trophoblast invasion - by, e. (factor-beta3 inhibitor, useful for detecting
                                                                                                                                                                       07-MAR-1997;
                                                                                                                                                                                                  05-MAR-1998;
                                                                                                                                                                                                                              17-SEP-1998
                                                                                                                                                                                                                                                          WO9840747-A1
                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                     preeclempsia;
                                                                                                                                                                                                                                                                                                                                                                                                   trophoblast invasion regulation; inhibitor; HIF-1 alpha; TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                Human transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid sequence of human hypoxia inducible factor 1 alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV63210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV63210 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 96-97; 103pp; English.
 preeclempsia in pregnant women
                                                         P-PSDB; AAW80418.
                                                                                                                            (HOSP-) HOSPITAL FOR SICK CHILDREN (MOUN ) MOUNT SINAI HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439
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                                                                     1998-520837/44.
                                                                                                                                                                                                                                                                                                                                                           sapiens.
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                                                                                                Lye
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                                                                                                                                                                                                                                                                                                                                                                                     pregnanancy; choriocarcinoma; ss.
                                                                                                                                                                      97US-0039919
                                                                                                                                                                                                  98WO-CA00180
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                                                                                                                                                                                                                                                                                   /*rag= a
/product= HIF-1 alpha
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  839
                                                                                                                                                                                                                                                                                                                                                                                                                          growth factor-beta 3; TGF-beta3; oxygen tension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.6%;
                                                                                                 Post
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                                                                                                 z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23.4; I
Pred. No. 0.19
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                648 T; 0
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                          e.g. transforming
                S,
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RESULT 5
AAD38995
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Best Local
risk of developing a haematol (MDR). The method involves ac (HIF-1) binding molecules or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-1lke-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes human hypoxia inducible factor 1 alpha (HIF-1 alpha). The specification describes a composition for regulating trophoblast invasion which comprises an inhibitor of transforming growth factor-beta 3 (TGF-beta3), TGF-beta family cytokine receptors, HIF-1 alpha or oxygen tension. The composition is used in methods of diagnosing, monitoring, preventing or treating conditions requiring regulation of trophoblast invasion, especially preeclempsia in pregnant
             The invention relates to a method of treating a subject having or at risk of developing a haematologic malignancy or multidrug resistance (MDR). The method involves administering hypoxia inducible factor-l
                                                                                                                Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia inducible factor 1 binding molecules or small
                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HIF-lalpha cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD38995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD38995
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                                                                                                    ubiquitin-like-modifier-1 binding molecules
                                                                                                                                                                                                                                                  (BGHM ) BRIGHAM & WOMENS HOSPITAL
                                                                                                                                                                                                                                                                                                            25-OCT-2001; 2001WO-US49856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polycythaemia vera; hypoxia responsive element; HRE; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3678 BP; 1197 A; 695 C; 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   women or choriocarcinomas.
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                                                                                                                                                                            2002-471427/50.
)B; AAE24212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig
                                                                         Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                               2000US-243542P
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                                                                          61-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.6%;
96.0%;
                                                                         92pp;
                                                                                                                                                                                                                                                                                                                                                                                                  "Human HIF-lalpha protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 0.
                                                                         English
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RESULT 6
ABK84257
AID 8428
AX ABK8
AX 
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The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening for an agent capable of modulating GCA or an inflammation 'contacting' (M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binding molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive element (HRR) binding molecules or antisense nucleic acid molecules and SUMO-1 binding molecules or antisense molecules are useful for treating a subject having or at risk of developing haematologic malignancy or MDR (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders include lymphocytic leukaemia or chronic lymphoroliferative disorders e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid disorders include chronic or acute myeloid leukaemia, e.g. angiogenic myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The invention is used in gene therapy. The present sequence is human HIF-lalpha cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS;
                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 838; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-435328/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beazer-Barclay Y, Weissman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2000; 2000US-237189P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ss; granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respiratory distress syndrome; 's disease; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA differentially expressed in granulocytic cells #838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENE LOGIC INC.
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96.0%;
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periodontal disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, ARDS, adult respiratory distress syndrome, reperfusion injury, ARDS, adult respiratory distress syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
                                      06-JUN-1995;
                                                                                                                  12-DEC-1996
                                                                                                                                                                                                                                                                                                   misc_signal
                                                                                                                                                                                                                                                                                                                                                                                               atherosclerosis; cerebral artery disease; gene
                                                                                                                                                                                                                                                                                                                                                                                                                  Hypoxia inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human hypoxia inducible factor-1 alpha cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the printed specification, but was obtained in electronic format directly from WIPO at
 (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED
                                                                           06-JUN-1996;
                                                                                                                                                     W09639426-A1
                                                                                                                                                                                                          polyA_signal
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT45937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT45937 standard; DNA; 3736 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3678 BP; 1197 A; 695 C; 675 G; 1111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 CCATGTGACCATGAGGAAATGAGAG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of expression in a sample of the tissue of gene(s) from Gs, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                        95US-0480473
                                                                           96WO-US10251
                                                                                                                                                                                                          3674..3679
                                                                                                                                                                                                                                               /function=
29..2509
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                           '*tag=
                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                             factor-1 alpha; HIF-1; tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human hypoxia inducible factor-1 (HIF-1), a DNA binding protein that binds to the enhancer region of e.g. erythropoletin and vascular endothelial growth factor (VEGF) genes. The DNA sequence is a composite of 3 clones obtd. by screening an Hep3B library and by database analysis. HIF-1 alpha nucleic acids can be used to prepare recombinant HIF-1 alpha in transformed host cells, as probes, and in the gene thorapy of HIF-1-mediated or hypoxia-related disorders such as atherosclerotic coronary or cerebral artery disease; antisense sequences inhibit HIF-1 expression e.g. to treat
                                                                                                                                                                                                       WO200010578-A1
                             WPI; 2000-246493/21.
P-PSDB; AAY69407.
                                                                                                                                                                                                                                                                                                                          Human: hypoxia-inducible factor 1 alpha; HIF-lalpha; variant; hypoxia inducible gene; hypoxia inducible factor; hypoxia; ischemia related damage; angiogenesis; coronary artery disease; ischemic tissue damage; ss.
                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding a wild type human hypoxia inducible factor-1 alpha
                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3736 BP; 1255 A; 695 C; 675 G; 1111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding human hypoxia-inducible factor enhancing expression of structural gene and
Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful
                                                                                                                         25-AUG-1998;
                                                                                                                                                  25-AUG-1999;
                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ99537 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour proliferation mediated by VEGF-induced angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A DNA sequence (AAT45937) codes for the alpha subunit (AAW06557) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypoxia-related tissue damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Semenza
                                                                                               (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Page 49-53; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GL;
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                        98US-0148547
                                                                                                                                                  99WO-US19416
                                                                                                                                                                                                                                                                                                                         damage;
                                                                                                                                                                                                                                                          Location/Qualifiers 29..2509
                                                                                                                                                                                                                              /*tag= a
/product= "hypoxia inducible
                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3736 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23.4;
Pred. No. 0
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treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                               factor-1 alpha"
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of
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RESULT 9
ABI99710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stable under hypoxic and non-hypoxic conditions. The variants comprise amino acid residues 1-391 and 521-826, 549-826, 576-826, 429-826, 469-826, 508-826, 508-826, 517-826 or 5
                 conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive
                                                                                                                                                                                                                                                                    Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                               The present invention describes a method for examining ischaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABI99710 standard;
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                                                                                                                                                                                            Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishikawa K, Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAY-2000; 2000JP-0145977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-2001; 2001WO-JP04192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vasospastic ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse ischaemic condition related cDNA sequence SEQ ID NO:759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating hypoxia or ischemia-related tissue damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 CCATGTGACCATGAGGAAATGAGAG 464
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                                                                                                                                                                                                                                                                                                                                                                                                                     2002-034733/04.
                                                                                                                                                                                                                                                                                                                                                                                           ABB57270
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                                                                                                                                                                                         Page 1863-1869; 2690pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA; 3746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi Y, Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ischaemic condition; ischaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishii Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
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ischaemia, occlusive ischaemia or vasospastic ischaemia) by

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RESULT 10
AAS61590
ID AAS61690
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                                                         amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient. (I), (II) or antigen-presenting cells expressing (II) is useful for stimulating and/or expanding T cells specific for a tumour protein. The method comprises contacting T cells
                                                                                                                                                                                                                                              The invention relates to novel isolated lung small cell cancer antigen polynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung tumour polynucleotide and polypeptides useful in therapy diagnosis of cancer especially lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-2000;
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytostatic; antitumour; lung small cell cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3746 BP; 1124 A; 740 C; 740 G; 1142 T; 0 other;
                                                                                                                                                                                     from the patient is contacted with (III), detecting the amount polynucleotide hybridised to (III) in the sample and comparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU69409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lung small cell carcinoma antigen, cDNA #231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS61690 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which are used in the exemplification of the present invention.
                                  with one of the components under conditions to permit the stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501
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   expansion of the cells. A composition comprising (I) is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-196780P.
2000US-213361P.
2000US-229763P.
2000US-230629P.
2000US-232565P.
2000US-257037P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-260796P
                                                                                                                                                                                                                                                                                                                                                                                                       201-202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mohamath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                       295pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70,
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            525
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                                                                                                                                                                                                                                                                                                              detecting
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AAX58980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                       to amplify additional flanking sequences from a commercial HepG2 library. MOP1 is also known as hypoxia inducible factor 1 alpha. The factor is induced by low oxygen. It interacts with HSP90 and with ARNT. The ARNT-dimerised factor regulates expression of erythropoietin, among other genes. The invention also provides novel MOPS 2-9 nucleic acids (see AAX58981-88) and proteins (see AAX06289-97). These are useful in a variety of research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stimulating an immune response in a patient and for inhibiting the development of a cancer especially lung cancer in a patient. An isolated T cell population is useful for removing tumour cells from biological sample and for inhibiting the development of cancer in a patient. AAS6180-AAS61874 represent novel human lung small cell cancer antigen coding sequences of the invention.
                                                                                                                                                                                     search of human ESTs designed to identify basic-helix-loop-helix-PAS (bHLH-PAS) proteins that interact with either the Ah receptor (AHR)
         diagnostic and therapeutic applications. alpha-class hypoxia-inducible factors.
                                                                                                                                                    or the Ah receptor nuclear translocator (ARNT). To obtain extended open reading frames for each EST, an anchored-PCR strategy was used
                                                                                                                                                                                                                 This is the nucleotide sequence of a cDNA encoding MOP1 (see AAYO6289), a member of the PAS superfamily, where PAS stands for PER/ARNIT/SIM domains. The cDNA was identified in an iterative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                 Developmental signal transduction associated proteins
                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY06289
                                                                                                                                                                                                                                                                                                                                                                                             Bradfield CA,
                                                                                                                                                                                                                                                                                                                                                                                                                             (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOP1; member of the PAS superfamily; bHLH-PAS; human; transcription regulator; hypoxia inducible factor 1 alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX58980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX58980 standard; cDNA; 3933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3927 BP; 1241 A; 782 C;
                                                                                                                                                                                                                                                                                  Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         670 CCATGTGACCATGAGGAAATGAGAG
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                                                                                                                                                                                                                                                                                Page 93-94; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Gu YZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0066863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 265..2745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulator MOP1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.6%;
96.0%;
                                                                                                                                                                                                                                                                                                                                                                                            Hogenesch JB,
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     748 G; 1156 T; 0
             Others are involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .21;
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                             Several of the MOPs are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
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                                                         The invention relates to isolated polynucleotide (I) and CD polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The complex compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3933 BP; 1243 A; 784 C; 750 G; 1156 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 20862; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #20862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS85058 standard; cDNA; 4162 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            676 CCATGTGACCATGAGGAAATGAGAG 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCATGTGACCATTAGGAAATGAGAG 25
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                                             ttp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene mapping; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Sequence 4162 BP; 1286 A; 843 C; 813 G; 1220 T; 0 other;

Q

1 CCATGTGACCATTAGGAAATGAGAG 25

Matches Query Match Best Local

Similarity

93.6%;

Conservative

0;

Pred. No. Score 23.4; Mismatches

0.24; DB 22;

Length 10355;

Indels

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ID AAS1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                     whose expression differs, by comparing expression under different environmental conditions. The method is useful for identifying mutations and polymorphisms that affect the biological response to a particular cellular process. The method also allows the molecular dissection of biological pathways by altering a particular pathway under study. By introducing a heterologous nucleic acid into a cell population, the level of a particular molecule can be influenced, allowing a pathway to be
                                dissected into its precise molecular components. The main use of the method is to compare gene expression in cells from a diseased patlent and from a normal patient. This sequence represents pSMART CMV-HIF from a vector expressing hypoxia inducible factor 1 alpha (HIF-1 alpha) which is used in methods of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                 Screening a genetic element involved in a cellular process, comprises comparing gene expressions in a cell, and a second cell that has altered levels of genes used in the process, and detecting an element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Differential expression; polymorphism; biological pathway; IRES; GFP; internal ribosome entry site; green fluorescent protein; HIF-1 alpha; hypoxia inducible factor 1 alpha; hypoxia regulated gene; macrophage;
Sequence 10355 BP; 3060 A; 2212 C; 2373 G; 2710 T; 0 other;
                                                                                                                                                                                                                                                  The invention relates to differential expression screening to identify genetic element involved in a cellular process. The method involves comparing gene expressions in two cells, where one cell has altered levels of a biological molecule, and identifying the genetic element
                                                                                                                                                                                                                                                                                                                                                                                with varied expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 psmarr cmv-Hif DNA from a vector expressing Hif-1 alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS14156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS14156 standard; DNA; 10355 BP
                                                                                                                                                                                                                                                                                                                                            Example 5; Page 97-101; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-589807/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kingsman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; CMV; cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    804 CCATGTGACCATGAGGAAATGAGAG 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000GB-0004197
2000GB-0018679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-GB00758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23.4; DB Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4162;
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                                                                                                                                               level
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RESULT 14
AAK77781 standard; D
XX
AAK77781;
XX
AXC
AK77781;
XX
AC
AK77781;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen
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2000US-0189350
2000US-0199350
2000US-019076
2000US-0190133
2000US-0205515
2000US-0216847
2000US-0216847
2000US-02114890
2000US-02145193
2000US-021963
2000US-0225964
2000US-0225214
2000US-0225214
2000US-0225214
2000US-0225214
2000US-0225214
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2000US-0225214
2000US-0225214
2000US-0225266
2000US-0225757
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2000US-0225758
2000US
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2000US-0180628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic sequence SEQ ID NO:32593.
         08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
14-SEP-2000
14-SEP-2000
14-SEP-2000
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14-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP
    2000US-0232398.
2000US-0232398.
2000US-0232398.
2000US-023398.
2000US-0233063.
2000US-0233063.
2000US-0233063.
2000US-0234297.
2000US-0234297.
2000US-0234297.
2000US-0235834.
2000US-0235834.
2000US-0235836.
2000US-0235836.
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2000US-0235836.
2000US-0236327.
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2000US-0236327.
2000US-0237039.
2000US-0237039.
2000US-024611.
2000US-0246476.
2000US-0246477.
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2000US-0246477.
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2000US-0246526.
2000US-0246611.
2000US-0246611.
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2000US-0246611.
2000US-0249211.
2000US-0249214.
2000US-024924.
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2000US-0232080
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ARESULT 15
AAH93977/G
ID AAH93
XX AAH93
XX AH93
XX O5-OC
DT 05-OC
XX Human
XX Human
XX Human
XX Human
XX gene
KW gene
KW gene
KW gene
KW gene
KW gene
XX nervc
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) concerns and polynucleotides may be used in the prevention, diagnosis and carefully, they may be used to treat disorders associated with decreased concerns and polynucleotides as associated with inappropriate (I) expression. For concerns a pattent's genome concerns and polynucleotides are to treat disorders associated with decreased concerns and polynucleotides are pattents or deletions in a pattent's genome consultation by rectifying mutations or deletions in a pattent's genome consultation by rectifying mutations of (I). Additionally, (I) concerns and the pattents own production of (I). Additionally, (I) concerns and cards into a host cell and culturing the cell to express the concerns and cancer metastases of haematopoletic-related diseases, especially concerns and cancer metastases of haematopoletic-derived cells. AAK64703 concerns and polynucleotides may be used to provent, and to a provent and cancer metastases of haematopoletic-derived cells. AAK64703 concerns and cancer metastases of haematopoletic-derived cells. AAK64703 concerns and polynucleotides are provent.
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                          26482 CCATGTGACCATGAGGAAATGAGAG 26458
                 Human; foetal protein; cytostatic; immunosuppressive; immunostimulant; nootropic; neuroprotective; thrombolytic; osteopathic; antiinflammator; gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder;
nervous system disorder; inflammation; expressed sequence tag; EST; ss
                                                                                                                                                          05-OCT-2001 (first entry)
                                                                                                                                                                                                                                 AAH93977 standard; cDNA; 367 BP.
                                                                                                                        Human foetal cDNA, SEQ ID NO: 506.
                                                                                                                                                                                                        AAH93977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27884 BP; 9296 A; 5084 C; 5260 G; 8244 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 32593; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                              1 CCATGTGACCATTAGGAAATGAGAG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0249299
2000US-0249300
2000US-0250160
2000US-0250391
2000US-0251030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0259678.
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2000US-0254097.
                                                                                                                                                                                                                                                                                                                                                                                                                     93.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                      0
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Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 27884;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                         antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                          0;
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Search completed: March 17, 2003, 10:50:36 Job time: 151.446 secs

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B
                                                             Matches
                                                                                      Query Match
                                                                                                                             The invention relates to novel foetal polypeptides encoded by polynucleotides comprising one of 477 sequences fully defined in the specification. The foetal polynucleotides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present sequence was assembled using an expressed sequence tag (EST) found to be expressed in human foetal tissue cDNA libraries as the seed.
                                                                                                        Sequence 367 BP; 94 A; 65 C; 58 G; 150 T; 0 other;
                                                                                                                                                                                                                                                               Claim 1; Page 362-363; 715pp; English.
                                                                                                                                                                                                                                                                                                  Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune disorders, growth disorders, thrombolytic disorders, nervous system
219 ATGTGACAATTAAGAATAAGAG 197
                                                                                                                                                                                                                                                                                                disorders and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                 Yeung G,
Liu C, A
                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAM06302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2000; 2000US-0491404
15-SEP-2000; 2000US-0663870
06-NOV-2000; 2000US-0707351
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2001; 2001WO-US02723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200155339-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                        3 ATGTGACCATTAGGAAATGAGAG 25
                                                                       ocal Similarity
                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                      2001-465571/50.
                                                                                                                                                                                                                                                                                                                                                                                                                 , Ford JE,
Asundi V,
                                                          Conservative
                                                                    72.8%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                             Boyle BJ, Arterbu
Zhou P, Werhman T;
                                                       0;
                                                                    Score 18.2;
Pred. No. 4
                                                      Mismatches
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                                                                             DB 22; Length 367;
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                                                   Indels
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-836-439-2
25
                                                                                                                                                                                                                                                                                                                                                                                                                            16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ccatgtgaccattaggaaatgagag 25
   GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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gb_gss:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

o u	0 4 w k	, _ ;	Result
23.4	23.4		
93.6 93.6	93.6 6	93.6	Query Match Length DB ID
395 501	380 386	337	ength
12 12	10	14	8
BE980521 BF406698	AW304323 AW120791 AW124493	93.6 337 14 BQ308862	ID
BE980521 UI-M-BG2- BF406698 UI-R-BJ2-	AW120791 UI-M-BH2. AW124493 UI-M-BH2.	BQ308862 MR0-BT550	Description

118 118 118 118 118 118 118 118 118 118	7 8 9 10 11 11 11 11 11 11 11 11 11 11
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889 893 941 1057 714 714 310 903 903 1435 478 601 1435 611 1435 611 622 335 633 633 644 648 648 648 648 648 648 648	591 684 711 734 739 769 791 878
114 114 114 114 110 110 110 110 1117 117 117 117 117 11	14 12 13 14 14
BE87724 BE87724 BO881947 BO881947 BM8077.53 AK017853 AK017853 AK017853 AV0131767 BB204614 AL598195 AX70482 BM906663 BQ306421 T31654 AQ010897 B90780 AZ263188 BQ39783 BB652302 BF617665 AZ778473 BM652302 BF617665 AZ77847 AQ10897 B907780 AZ263194 AQ10897 B907780 AZ263198	A1481068 BM834484 BB19902 BE731662 BE789080 BI413382 BF7897 BG110077 AU132294 BG7711945
BEST7744 GENCOURT BEST7744 GOLVENTOURT BEST7744 GOLVENCOURT BM807153 AGENCOURT BM007153 AGENCOURT BM007153 AGENCOURT AK017853 MUS muscu AU131767 AU131767 BB204614 BB204614 AL598195 DKRZP6860 AZ786928 2M0032N05 W86995 zh61e02.s1 AA700482 zj74f07.s BM906863 AGENCOURT BO308421 KR0-BT450 T31654 EST36504 Hu AQ108979 CITY-HSP-217 AZ263188 RPCI-23-1 BQ397883 NISC_mo02 BB652302 BB652302 BF617665 HVSMEC001 AZ778470 ZM0013K17 BJ198294 BJ198294 AZ433190 1M0218L22 BJ198711 BJ195711 AZ931901 474.dhz91 AL184121 TELTBOOG AZ03974 MJ28905.r BM482542 535462 MA BH026082 RPCI-24-3	

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ALIGNMENTS

0 0 0 0 0 0 0

	JOURNAL MEDLINE COMMENT	TITLE	REFERENCE AUTHORS	VERSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BQ308862 LOCUS DEFINITION
Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001	sequence rags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663 Contact: Simpson A.J.G.	Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.	Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Eutereoscomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 337) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,	BQ308862.1 GI:20851208 EST. human. Homo sapiens	B0308862 B0308862 337 bp mRNA linear EST 16-MAY-2002 MRO-BT5505-040701-003-c02 BT5505 Homo sapiens cDNA, mRNA sequence.

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                             Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eco RI site shown at the beginning of the sequence Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 348) NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MRO&t2=MRO-BT5505-040701-003-c02&t3=2001-07-04&t4=1)
Seq primer: puc 18 forward
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/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco
/notructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided)
                                                                                                        /cell_type="germinal center B cells"
/cell_line="MGC85"
                                                                                                                                                   /clone_lib="NIH_MGC_50"
/tissue_type="lymph"
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/clone="IMAGE:3079736"
                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/dev_stage="Adult"
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mEST@mail.nih.gov
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/dev_stage="27-32 days"
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/clone="UI-M-BH2.3-any-h-05-0-UI"
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/strain="C57BL/6J"
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Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
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                                                                                                                                                                                                                                                                                                                   Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized amygdala library CDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the updated accordingly when that means is determined.
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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TAG_LIB-NIH_BMAP_M_S3.3
TAG_TISSUB-bhasal-ganglia
                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH2.1-apo-a-05-0-UI"
/clone_lib="NIH_BMAP_M_S3.1"
/dev_stage="27-32 days"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                          /lab_host-"DH10B (Life Technologies)"
                                                                                                                                                                                                   /organism-"Mus musculus"
                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.4;
Pred. No. 2.
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COMMENT

JOURNAL MEDLINE TITLE AUTHORS

REFERENCE

SOURCE KEYWORDS VERSION ACCESSION DEFINITION AW124493 RESULT 4

ORGANISM

BASE COUNT

Matches

FEATURES

COMMENT

REFERENCE

AUTHORS

TITLE JOURNAL

SOURCE KEYWORDS ACCESSION DEFINITION

ORGANISM

VERSION

source

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Query Match
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Local Similarity 96.0%;
Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the amygdala tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 395)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE980521 395 bp mRNA linear EST 05-OCT-200 UT-M-BG2-bck-b-03-0-UI.Sl NIH_BMAP_MSC_Sl Mus musculus cDNA clone UI-M-BG2-bck-b-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_TISSUE=amygdala
TAG_SEQ=GTGAG"
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Pred. No. 2.
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RESULT 5 BE980521

ocus

ORIGIN BASE COUNT

Matches

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF406698 501 bp mRNA linear EST 28-NOV-
UI-R-BJ2-bpo-b-02-0-UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone
UI-R-BJ2-bpo-b-02-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                          Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.ccm) The following repetitive
elements were found in this cDNA sequence: 25-96, >BI-F#SINE/Alu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Bckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                             POLYA-No.
                                                                                                                                                                                                                                                                          Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer: M13 Forward
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/lab host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note:-pT7T3D-Pac (Pharmacia) with a modified
/note:-pT7T3D-Pac (Pharmacia) with a modified
/note:-pT7T3D-Pac (Pharmacia) with a modif
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1 73 c
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TAG_LIB=NIH_BMAP_MSC_S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="UI-M-BG2-bck-b-03-0-UI"
/clone_lib="NIH_BMAP_MSC_S1"
/dev_stage="27-32 days"_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_TISSUE=amygdala
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/strain="C57BL/6J"
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ2-bpo-b-02-0-UI"
                                                                                                                        /organism="Rattus norvegicus"
                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lennon, G. and Soares, M.B.
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AT481068 591 bp mRNA linear EST 09-MAR-1999 vf92d03.x1 Soares_mammary_gland_NDMMG Mus musculus CDMA clone IMAGE.851237 3' similar to TR:008741 008741 HYPOXIA-INDUCIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 591)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on wrong strand High quality sequence stop: 472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone was previously sequenced on the 5' end only, this new data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:503389
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/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lote="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: ptroperation of the properation of the properation of the properation of the properation of the library from which this clone was derived, please
visit our web site at ratest.eng.uiowa.edu. The
subtraction has been previously described in (Bonaldo,
Lennon and Soares, Genome Research 6:791-806, 1996)

Lennon and Soares, Genome Research 6:791-806, 1996)
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100 c 125 g
T 3/]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                           /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:851237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                               note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco
                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_mammary_gland_NbMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain-"C57BL/6J"
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                                                                                                                                                                               th a modified polylinker; Site_1: Not I; Site_2: Ec 1st strand cDNA was primed with a Not I - oligo(dT)

 Mismatches

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Pred. No. 3.2;
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BM834484
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: yongsung@mail.kribb.re.kr
Plate: 63 row: B column: 11
High quality sequence stop: 684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 684)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Korea Research Institute of Bioscience & Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-EST0109485 S11SNU1 Homo sapiens cDNA clone S11SNU1-63-B11 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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        Conservative
                                                                                                              Indice Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI; Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Sfil site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using Sfil oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with Sfil and cloned into DraIII- digested pME185-FL3 vector. The competent cells E. coli ToplOF by electroporation method. The CDNA vectors were used for transformation of the cDNA libraries constructed by this method are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Lymphoblast-like"
/cell_line="SNU-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="$11$NU1-63-B11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="Top10F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Stomach"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="S11SNU1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Homo sapiens"
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                        93.68;
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      0,
                        Score 23.4; DB 14; Length 684; Pred. No. 3.6;
                                                                                                         136 g
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Pred. No. 3.
    Mismatches
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                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Hiramoto,K., Hori,F., Ishli,Y., Ito,M., Kawal,J., Konno,H., Kouda,
M., Koya,S., Matsuyama,T., Miyasaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
                                                                                                                                                                                                                                           prepare mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Klyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN integrated sequence analysis (RTSA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
On Jun 30, 2000 this sequence version replaced g1:8864855.
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB199902 RIKEN full-length enriched, O day neonate thymus Mus musculus cDNA clone A430018A13 3', mRNA sequence.
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\c/clone\_lib="RIKEN full-length enriched, 0 day neonate thymus"
                                                                       /clone="A430018A13"
                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
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414 CCATGTGACCATGAGGAAATGAGAG 438
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                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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High quality sequence stop: 697.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/dev_stage="0 day neonate"
/lab_host="DH10B"
/tissue_type="choriocarcinoma"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
poliowing 5' adaptor: GGCACGAG(G). Size-selected >500bp
following 5' adaptor: GGCACGAG(G). Library constructed by
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_21"
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96.0%;
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REFERENCE

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                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                 CCATGTGACCATGAGGAAATGAGAG 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9810 row: p column: 09 High quality sequence stop: 708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602104940F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5', mRNA sequence
BF789080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF789080.1 GI:12094116
                                                          BI413382
                                                                                           B1413382 739 bp mRNA linear EST 14-AUG-2001 602986733F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5142800 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nouse mouse
                                     BI413382.1 GI:15174305
                                                                          mRNA sequence
house mouse
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                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Kid14"
/lab_host="NCI_CGAP_Kid14"
/lab_host="PH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pcMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
/site_2: Sall; Cloned unidirectionstructed by Life
/Average insert size 1.75 kb. Constructed by Life
/Technologies. Note: this is a NCI_CGAP Library. | "

a 147 c 170 g 200 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:4223096"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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Pred. No. 3.6
                                                                                                                                                                                                                                                                                                                   Score 23.4; DB 12; Pred. No. 3.7;
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COMMENT
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BG772697
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 681 CCATGTGACCATGAGGAAATGAGAG 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RKEN)
                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 769)
                                                                                                                                                                                                                                                                                                 BG772697 769 DP MKNA LINCOL 100 602720844F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4837691 5',
                                                                                                                                                                                                                                                                       BG772697.1 GI:14083350
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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High quality sequence stop: 726.
Location/Qualifiers
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DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11352 row: a column: 09
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Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="CZECH II"
/db_xref="taxon:10000"
/clone="IMAGE:5142800"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.4; DB 13; Length 739; Pred. No. 3.7;
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FEATURES
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10019 row: e column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Emmall: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                         High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 791)
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10770 row: h column: 12
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/organism="Homo saplens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4367229"
/clone_1ih="NIH_MCC_86"
/tissue_type="osteosarcoma, cell line"
/tissue_type="osteosarcoma, cell line"
/lab_host="HIOB (phage-resistant)"
/note="Organ: bone; Vector: pCMV-SpORT6; Site_1: Not;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Togan: testis; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

a 143 c 170 g 213 t
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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96.0%;
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Pred. No. 3.8;
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Search completed: March 17, 2003, 13:09:12 Job time : 888.737 secs
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                                                                                                                                                   Y Match 93.6%; Score 23.4; DB 9; Length 878; Local Similarity 96.0%; Pred. No. 4; Local Similarity 96.0%; Pred. No. 4; Prodels 1: Todels 1: Todels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genomics@hri.co.jp
HRI human cDNA project; 5'. & 3'.end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRI human cDNA project
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Contact: Takao Isogai
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 878)
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Pred. No. is the number of results predicted by chance to have a

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Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs

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ALIGNMENTS

	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AF249160	RESULT 1
Bossuyt, F. and Milinkovitch, M.C.	1 (bases 1 to 175)	Philautus.	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Philautus charius	Philautus charius.		AF249160.1 GI:12247249	AF249160	, exon 4 aı	AF249160 175 bp DNA linear VRT 17-JAN-2001		

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Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
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Archer, S.N. and Hirano, J.
Comparative analysis of c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 175)
Bossuyt, F. and Milinkovitch, M.C.
Direct Submission
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/db_xref="taxon:27697"
/tissue_type="retina"
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Kawamura, S., Blow, N.S. and Yokoyama, S. Genetic analyses of visual pigments of the pigeon (Columba livia) Genetics 153 (4), 1839-1850 (1999)
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/note="degenerate primer"
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                                                                                                                                                                                                                                         transmembrane helix prediction.

And the sequence is submitted by the collaborative project between [Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST)] and [Genome Science Division, Research Center for Advanced Science and Technology (RCAST), University of Tokyo].
                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-701-2001) Makiko Suwa, Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/, Tel:81-3-3599-8080, Fax:81-3-3599-8081) www.cbrc.jp/, This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automated system that contains programs of gene finding(GeneDecoder), sequence search, motif-domain assignment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suwa, M., Sato, T., Okouchi, I., Arita, M., Futami, K., Matsumoto, S., Tsutsumi, S., Aburatani, H., Asai, K. and Akiyama, Y. Genome-wide discovery and analysis of human seven transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Dryja.T.P. and Berson,E.L.
Diagnosis of hereditary retinal degenerative diseases
Patent: US 5498521-A 1 12-MAR-1996;
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/evidence=not_experimental
/product="seven transmembrane helix receptor"
/protein_id="BACOS894.1"
/db_xref="GI:21928611"
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/chromosome="3"
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Submitted (22-FEB-1996) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205, USA
On Sep 3, 1996 this sequence version replaced gi:189393.
                                                                            Direct Submission
                                                                                           Nathans,J
                                                                                                                                           84272729
                                                                                                                                                                      rhodopsin
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Dryja,T.P. and Berson,E.L.
Diagnosis of hereditary retinal degenerative diseases
Patent: US 5498521-A 2 12-MAR-1996;
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Sequence 2 from patent US 5498521.
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FLLIULGFPINELTLYVTVOHKKLRTPLNYILLAVADLFWLJGGFTGSTLYTSLHGY
FVFGPTGCNLEGFFATLGGEIALMSLVVLAIERVVVVCSPMSNRFGSRHVTHAIMOVAFT
WYMALACAAPPLAGWSRYIPEGLGCSCGIDYYTIKPEVNNESFVIYMFVVHFTIPMII
IFFCYGQLYFTVKEAAAQQGESATTQKAEKEVTRMVILMVIAFLICWVPYASVAFYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="rhodopsin mRNA (alt); the 5' untranslated region is similar to the bovine sequence" join(295. .655,2439. .2607,3813. .3978,4095. .4334,5168. .5278) /note="the 5 exons of the human rhodopsin gene are similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="rhodopsin mRNA (alt); the 5' untranslated region is similar to the bovine sequence"
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/isolate="individual J.N."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="intron A; the four introns present in both the human and the bovine genes occur at precisely analogous positions and are of comparable lengths"
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ATVSKTETSQVAPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAC31763.1"
/db_xref="GI:1236137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the 5 exons of the Bos taurus opsin gene"
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5642. .56
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                                                                                                                                                                                                                                                                                                                    /note="potential polyA signal"
6698. 6903
/note="potential polyA signal"
1 2022 c 1796 g 1611 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="intron C; the four introns present in both the human and the bovine genes occur at precisely analogous positions and are of comparable lengths"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="rhodopsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human and the positions and
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/note="intron
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                                                                                                                                                                                                        89.2%;
95.7%;
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                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACO23162 163297 bp DNA linear HTG 24-JUL-2002
Homo sapiens chromosome 3 clone RP11-26311, WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                               Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                      Submitted (09-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                 Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C.
                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                   Jul 19, 2002 this sequence version replaced gi:20127313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 163297)
Contact: hgsc-help@bcm.tmc.edu
                        web site: http://www.hgsc.bcm.tmc.edu/
prafting Center Code: BCM
                                                                                      Center code: BCM
                                                                                                     Center: Baylor College of Medicine
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REFERENCE
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                                                             (bases 1 to 164396)
Evans G.A., Bradbury, P., Brignac, S., Bumeister, R., Davie, J.,
Davies, C.J., Davis, C., English, C., Fondon, T., Franklin, T.L.,
Garner, H.R., Gordon, M., Gotway, G., Grant, O., Hahner, L., Harris, J.,
Hinson, S., Megarity, C., Narayanaswamy, U., Newton, J., O'Brien, K.,
Oliver, T., Patel, P., Probst, S., Rayner, S., Schageman, J.,
Schilling, P., Schultz, R., Syed, M., Valenzuela, D., Ward, T.,
Wilson, R. and Burbee, D.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
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Center clone name: RP11-26311
Center clone name: RP11-26311
Sequencing vector: Plasmid,
Sequencing vector: M13;
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57018
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2733: gap of unknown length
22721: contig of 19988 bp in length
22821: gap of unknown length
57017: contig of 34196 bp in length
57117: gap of unknown length
16297: contig of 106180 bp in length.
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95.7%; Pred. No. 11
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RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankeaburg, K., Bonin, D., Bouck, J., Bowie, S., Bieve, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Garll, R., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hartis, C., Harris, K., Hart, M., Hale, S., Hale, X., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
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1 (bases 1 to 168551)
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On Jun 13, 2002 this sequence version replaced gi:1907283.
* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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Evans,G.A., Bradbury,P., Brignac,S., Bumeister,R., Davie,J.,
Davies,C.J., Davis,C., English,C., Fondon,T., Franklin,T.L.,
Garner,H.R., Gordon,M., Gotway,G., Grant,O., Hahner,L., Harris,J.,
Hinson,S., Megarity,C., Narayanaswamy,U., Newton,J., O'Brien,K.,
Oliver,T., Patel,P., Probst,S., Rayner,S., Schageman,J.,
Schilling,P., Schultz,R., Syed,M., Valenzuela,D., Ward,T.,
Wilson,R. and Burbee,D.
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38527 a 43485 c 42989;
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95.7%;
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Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karisson, E., Kelly, S., Khan, U., King, L., Korvah, J., Lewis, L., Li, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lewis, L., Li, J., Li, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lorier, R., Lucier, R., Martindale, A., Martinez, E., Massey, E., Maybua, P., Mattin, R., Martindale, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., McLeod, M.P., Meador, M., Moore, S., Morgan, M., Moorish, T., McLeod, M.P., Meador, N., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguye Direct Submission

REFERENCE TITLE JOURNAL TITLE AUTHORS JOURNAL

Unpublished 2 (bases 1 Direct Submission Worley, K.C. (bases 1 to 168551)

Submitted (23-SEP-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE AUTHORS (bases 1 to 168551)

Worley, K.C.

TITLE

JOURNAL Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE AUTHORS

JOURNAL

COMMENT

gc-help@bcm.tmc.edu

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

Submitted (07-MAR-2002) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On NOV 30, 2001 this sequence version replaced gi:16572867. Submission Department

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are o sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the clones are only ne remainder of

ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550) searc of a local database that includes entries from dbSTS, GDB, and 7:541-550) searches

local mapping efforts.

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. standards - estimated error rate less than 1 per 10,000 bases reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

FEATURES repeat_region repeat_region repeat_region repeat_region source repeat_region QUALSTAT-REPORT /rpt_family="MIR" 5772. .5848 /rpt_family="MIR" 3181. .3356 complement(2297. complement(1767. .2096)
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                                                                                                                                                                                Submitted (14-APR-1997) Molecular Genetics, Ophthalmology, Bath
Street, London ECIV 9EL, UK
                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                        Hunt, D.M., Fitzgibbon, J., Slobodyanyuk, S.J., Bowmaker, J.K. and
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Mol. Phylogenet. Evol. 8 (3), 415-422 (1997)
                                                                                                                                                                                                                                                                                                                                   Molecular evolution of the cottoid fish endemic to Lake Baikal
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                                                                                                                       /organism="abyssocottus korotneffi"
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                                                                                               /codon_start-1
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AF249133.1 GI:12247195
                  Mantella madagascariensis rhodopsin gene, exon 4 and partial
                                            AF249133
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute of Molecular Biology and Medicine, rue Jeener and Brachet 12, Gosselies B-6041, Belgium Location/Qualifiers
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Bossuyt,F. and Milinkovitch,M.C.
Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits
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a 48 c
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/protein_id="AAG49773.1"
/db_xref="GI:12247190"
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                                                                                                                                                                                                                                                                                  /translation="AEKEVTRMCIIMVVFFCISWFPYAFVAFWIFTHQGSEFGPIFMT
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/db_xref="taxon:143655"
<1. .>175
                                                                                                                                                                                                                                                                                                                                                     /codon_start=2
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KEVSRMYVIMVIGELVCWLPYASVAWWIFCNQGSDEGPIFMTLPSFFAKSAAIYNPWI
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
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Bossuyt,F. and Milinkovitch,M.C.
Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
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/protein_id="AAG49776.1"
/db_xref="GI:12247196"
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/product="rhodopsin" <1. .>175
                                                                                 /organism="Mantidactylus of. ulcerosus"
/db_xref="taxon:129014"
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BASE COUNT
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                          1 GCTTTCTTTGCCAAGAGCGCCGC 23
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                                                                                                                                                                                                                                                                                                                                       Bossuyt,F. and Milinkovitch,M.C. Direct Submission Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute of Molecular Biology and Medicine, rue Jeener and Brachet 12, Gosselles B-6041, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF249136.1 GI:12247201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bossuyt,F. and Milinkovitch,M.C. Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs Reveal Co-variation between Larval and Adult Traits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boophis xerophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                        Conservative
                                                                                                                           34 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPAFFAKSSAIYNP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAG49777.1"
/db_xref="GI:12247198"
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<1. .>175
                                                                                                                             /number=4
a 55 c
                                                                                                                                                                                                                                                                                                    /organism="Boophis xerophilus"
                                                                                                                                                                  VPAFFAKSSAIYNP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.5%;
91.3%;
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                                                                                                                                                       .>175
                                                                        82.5%;
91.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 g
                                                                       Score 19.8;
Pred. No. 37
                                                           0; Mismatches
                                                                                                                               34 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 t
                                                                              37;
                                                                                                                                  52 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                           Length 175;
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRT 17-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:
3 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:
4 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:
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25 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gctttctttgccaagagcgccgca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            March 17, 2003, 09:42:12; Search time 137.548 Seconds (without alignments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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/SIDS2/gcgdata/geneseg/geneseqn-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392.938 Million cell updates/sec
HHLHDO# GE
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Result	O	Query	Query Match Length DB 1	DB	ID	Description
	21.4	89.2	3016	17	AAT17115	Rhodons to dono
N	21.4	89.2	6953	17	AAT17116	phodopoti yelle. I
w	18.8	78.3	8641	20	AAX84344	stoodorn gene. n
4	18.2	75.8	3129	14	AAO4 3543	oreatri vilus nuci
Ų.	18.2	75.8	3190	23	ABL26876	Processia delle.
0	17.6	73.3	1563	21	AAZ53713	Notes of the metallog
	17.4	72.5	2209	22	AAS41923	denomic segment to
0	17.4	72.5	2601	20	AAX90036	Forwide bedreit
0	17	70.8	36135	22	AAK84218	Human immune/haema

	G	O	C		G	O	O	O	C	C	C	C	O	O	O	O	C	a	O								a	a								
	<u>4</u>	44	4	42	41	40	39	38	37	36	ü	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
	16.2		16.2		16.2						16.4		16.4		16.4	16.4		16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.8	16.8	16.8	16.8	
	67.5	67.5	67.5	67.5	67.5	67.5	67.5	68.3	68.3	68.3	68.3	68.3						N	N								69.2							70.0		70.0
	586	563	493	485	459	395	392	5801	2060	2060	2013	956	433	c385	385	337	3 36	240825	34185	4785	4785	4785	4785	4785	4785	4785	1845	795	740	408	408	4446	2304	1679	506	467
	22	24						21	23	23	22	22	21	23	23	23	23	22	21	14	14	14	14	14	12	12	17	24	22	24	24	23	23	24	23	23
AT TO MENTS	AAL22800	ABN73103 .	AAA57090	AAH84028	AAL13938	ABV06135	AAA57072	AAZ93310	ABV28314	ABV22500	ABA18522	ABA12912	AAA44043	ABV42957	ABV34093	ABV12971	ABV03802	AAF24497	AAC62130	AAQ48797	AAQ48796	AAQ48795	AAQ48794	AAQ48788	AAQ14942	AA014072	AAT33631	ABNA6622 ·	AAK59608	ABK80749	ABK80729	ABL02990	ABL02991	373	59	ABV12459
	Human breast cance	embry.	Human colon cancer	Enleman fulving olf	Himan broact care			מפוופת היספרמרם פאף	בייייים רפונפ	DEL VOIS		Sect etec	בי טייים רפירפ	ייייייייייייייייייייייייייייייייייייייי	prostate or or care	מייים לייים לייים	nroetate					B Obbenete Car/189		B Obbensia mitart	Cyclodestrin gluca	Teorga tatage	Streptococcus poly	imman immune/ndema	Himan (mmino/hacma		100000	Drosophile molesco		Rat garmanca diffic	prostate Prostate	1

ALIGNMENTS

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RESULT 1
AAT17115
                                         misc_binding
                                                                                                                                 5'UTR
                                                                                                                                                                                           Human; rhodopsin; transversion; mutation; retinitis pigmentosa; probe; primer; hybridisation; polymerase chain reaction; PCR; eye; rod; retina; diagnostic; prenatal diagnosis; photoreceptor; ds.
                                                                                                   primer_bind
                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                     Rhodopsin gene.
                                                                                                                                                                                                                                                         06-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                               AAT17115 standard; DNA; 3016 BP
                                                                                        /*tag= b
/note= "Alternative 5'-UTR"
complement (231..250)
                                                                                                                             /*tag= 8
202..294
/*tag= e
/note= "Binds probes AAT17117 (mutant) and AAT17118
  (normal)"
                                      /product= Rhodopsin complement (354..372)
                                                             /*tag= c/note= "Binds primer 348 (AAT17121)"
295..5278
                                                                                                                                                 Location/Qualifiers 200..294
                                                            /*tag= d
```

mutation

primer_bind

US5498521-A

misc_binding

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pigmentosa. Probes AAT17117 and AAT17119 bind to the C-to-A pigmentosa. Probes AAT17117 and probes AAT17118 and AAT17120 bind transversion mutation sequence, and probes AAT17118 and AAT17120 bind to the corresponding normal sequence. Primers 485 (AAT17122) and 502 (AAT17123) may be used along with primer 348 (AAT17121) to amplify mutant and normal sequences, respectively, by PCR. Mutations in the retinal degeneration slow protein and retinal rod cGMP-phosphodiesterase genes are also implicated in retinitis pigmentosa. Detection of any of these mutations in a foetus or
                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes human rhodopsin, and is shown without introns. The full sequence, with introns, is shown in AAT17116. Substitution of histidine for the normal nonpolar amino acid proline at position 23, by substitution of C with A in codon-23, results in a dysfunctional or absent molecule, affecting rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosis of hereditary retinal degenerative diseases e.g. retinitis pigmentosa, - caused by a human photoreceptor protein mutation, by detection of the mutation by PCR amplification or hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR93116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-159684/16.
                                                                                                                                                                                                                                                                   Sequence 3016 BP; 689 A; 863 C; 753 G; 711 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Column 19-24; 71pp; English.
    Rhodopsin gene
                                                                                                                                                                                                                                                                                               patient may be used in diagnosis.
                                                                                     AAT17116 standard; DNA; 6953 BP
                                                                                                                                                                                    1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                        GCGTTCTTTGCCAAGAGCGCCGC 1190
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dryja TP;
                                                                                                                                                                                                               Conservative
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0033081.
90US-0469215.
91US-0805123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0469215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= g
/note= "Substitution with A in mutant sequence"
362..381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Binds probes AAT17119 (mutant) and AAT17120 (normal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (355..369)
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Binds primers 485 (AAT17122) (normal) and 502
                                                                                                                                                                                                                             89.2%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (mutant)"
                                                                                                                                                                                                                0;
                                                                                                                                                                                                                             Score 21.4; DB 17; Length 3016; Pred. No. 1.7;
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                    0;
Human; rhodopsin; transversion; mutation; retinitis pigmentosa; intron; probe; primer; hybridisation; polymerase chain reaction; eye; rod; retina; diagnostic; prenatal diagnosis; photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                11-MAR-1993;
24-JAN-1990;
11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation
                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intron
WPI; 1996-159684/16
                                                                                                                                        24-JAN-1990;
                                                                                                                                                                    12-MAR-1996
                                                                                                                                                                                             US5498521-A
                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                           Berson EL, Dryja TP;
                                                    (HARD ) HARVARD COLLEGE.
                                                                                  93US-0033081.
90US-0469215.
91US-0805123.
                                                                                                                                        90US-0469215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (355..369)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (354..372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (231..250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/note= "Alternative 5'-UTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 200..294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number= j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number= 1
2439..2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362..381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /noté= "Binds probes AAT17119 (mutant) and AAT17120 (normal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "Binds probes AAT17117 (mutant) and AAT17118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Binds primer 348 (AAT17121)"
295..655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                666..2438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "Binds primers 485 (AAT17122) (normal) and 502
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                                                                                                                                                                                                                                                                                                           /number= 4
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"Substitution with A in mutant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (mutant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence"
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AAT17116 ID AAT1

XEXTXXX

06-JUL-1996 AAT17116; Вp δÃ

1168

Query Match Best Local : Matches

Berson EL,

11-DEC-1991; 24-JAN-1990; 11-MAR-1993; 24-JAN-1990; 12-MAR-1996

P-PSDB; AAR93116

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Best Local
This sequence represents a Stealth virus nucleic acid clone. The invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with probe from a known stealth virus and sequencing the resultant isolated nucleotide. The method comprises the steps of: (a) isolating DNA or RNA
                                                                                                         Claim 19; Page 76-79; 95pp; English.
                                                                                                                                            Novel strains of stealth virus
                                                                                                                                                                                WPI; 1999-405521/34.
                                                                                                                                                                                                                                                (MART/) MARTIN W J.
                                                                                                                                                                                                                                                                                30-DEC-1997;
                                                                                                                                                                                                                                                                                                               30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                            Stealth virus.
                                                                                                                                                                                                                                                                                                                                                                                                                               Stealth virus; detection; diagnosis; infection; ss
                                                                                                                                                                                                                                                                                                                                                                             W09934019-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stealth virus nucleic acid clone, SEQ ID NO: 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX84344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX84344 standard; DNA; 8641 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4272 GCGTTCTTTGCCAAGAGCGCCGC 4294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transversion mutation sequence, and probes AAT17118 and AAT17120 bind to the corresponding normal sequence. Primers 485 (AAT17122) and 502 mutant and normal sequences, respectively, by PCR. Mutations in the retinal degeneration slow protein and retinal red CGMP-phosphodiesterase genes are also implicated in retinitis partiant man be used in a foetus or constant and retinities are also implicated in a foetus or constant and retinities are the results of these mutations in a foetus or constant and retinities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6953 BP; 1523 A; 2022 C; 1797 G; 1611 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           patient may be used in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon 23, results in a dysfunctional or absent molecule, affecting rod function, and is linked with autosomal dominant retinitis pigmentosa. Probes AAT17117 and AAT17119 bind to the C-to-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes human rhodopsin, and is shown in full with introns. The corresponding sequence without introns is shown in AATI7116. Substitution of histidine for the normal nonpolar amino acid proline at position 23, by substitution of C with A in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosis of hereditary retinal degenerative diseases e.g. retinitis plymentosa, caused by a human photoreceptor protein mutation, by detection of the mutation by PCR amplification or hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Column 23-30; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                          97US-0001184.
                                                                                                                                                                                                                                                                                                           98WO-US27744.
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95.7%;
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Pred. No. 2;
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versions of this sequence encode proteins which cause retinal degeneration. These sequences may be identified using primers/ probes described in the invention (see also AAQ43545-48) and may be used to diagnose hereditary retinal degeneration. This sequence is the closest approximation to the gene sequence as the sequence given in the specification is not printed clearly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                       The sequence given represents the human rhodopsin cDNA.
                                                                                                                         Disclosure; Fig 1; 56pp; English.
                                                                                                                                               Probe or primer contg. sequence of human retinal degeneration slow protein mutant - used to diagnose hereditary retinal degenerative diseases
                                                                                                                                                                                                                                                        Berson EL, Dryja TP;
                                                                                                                                                                                                                                                                                     (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                 11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                             08-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8149 CTTTCTTTCGCAAGAGCGCCGC 8170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from a sample suspected of containing a stealth virus, e.g. a culture of ceils showing a viral cytopathic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 identified from a stealth virus; and, optionally (c) sequence previously isolated DNA or RNA molecules that react with the probe. The method is environment. The method is also used to detect stealth virus in a biological product, food or in the inhibitory or stimulatory effects on stealth virus replication and to determine capacity of the virus to recombine with and potentially alter the nucleic acid sequences of a cell or bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hereditary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhodopsin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-NOV-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ43543 standard; cDNA; 3129 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8641 BP; 2101 A; 2031 C; 2018 G; 2476 T; 15 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                              1993-214088/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rhodopsin; mutant; retinal degeneration; primer; probe;
                                                                                                                                                                                                                   AAR38483
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                                                                                                                                                                                                                                                                                                              91US-0805123
                                                                                                                                                                                                                                                                                                                                          92WO-US10536
                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
295..13
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Pred. No. 3
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                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1168 GCGTTCTTTGCCAAGTCCGCCGC 1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL26876;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB7737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 32101; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                          specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                     Sequence 3190 BP; 831 A; 719 C; 649 G; 991 T; 0 other;
                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                  2504 CTTTCTTGGCCAAGAGTGCAGCA 2526
                                                                                                                                          Local
                                                                           2 CTTTCTTTGCCAAGAGCGCCGCA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                      1 Similarity
20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M,
                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.8%;
87.0%;
                                                                                                                                               75.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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 Mismatches

                                                                                                                                                 Score 18.2;
Pred. No. 61;
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                                                                                                                                                                          DB 23; Length 3190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention is
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ID AAS4
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                                           RESULT 7
                                                                                                                                                                                            Matches
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02-SEP-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ53713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria gonorrheae ORF 506 partial DNA sequence SEQ ID NO:1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial; gene therapy; ds.
                                                                                                                                                                                                                                                                                                            AAX53015 to AAX54536, AAX54577 to AAX54615, and AAY74253 to AAY75941 and polypeptides. AAX54537 to AAX54576 and N. gonorrheae polypucleotides and polypeptides. AAX54537 to AAX54576 and AAX54616 to AAX55473 represent primers used in the exemplification of the present invention. The polypucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as the inmunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to manufacture of medicaments for treating or preventing infection due to presence of Neisseria bacteria, or to raise antibodies. They may also presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves be used as antibacterial agents. The polyucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria gonorrheae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics
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                                                                                                                                                                                                                                                                          Sequence 1563 BP; 287 A; 372 C; 487 G; 417 T; 0 other;
    AAS41923 standard; DNA; 2209 BP
                                                                                                          63 GCTTTGTTTGACAACACCGCCGCA 40
                                                                                                                                                 1 GCTTTCTTTGCCAAGAGCGCCGCA 24
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                                                                                                                                                                                                              h 73.3%; Score 17.6; DB 21; Length 1563; Similarity 83.3%; Pred. No. 1.1e+02;
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                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0103749.
98US-0103794.
98US-0103796.
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98US-0099062.
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 Mismatches

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Scarselli
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AAZ53713/c RESULT 6 IJ

AAZ53713 standard; DNA; 1563 BP

AAS41923;

Gaps

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06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 10-SEP-2000 12-SEP-2000 14-SEP-2000	14-AUG-2000 18-AUG-2000 22-AUG-2000 22-AUG-2000 23-AUG-2000 23-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000	11-JUL-2000; 11-JUL-2000; 14-JUL-2000; 26-JUL-2000; 26-JUL-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000;	31-JAN-2000 04-FEB-2000 24-FEB-2000 02-MAR-2000 11-MAR-2000 11-MAR-2000 11-MAY-2000 07-JUN-2000 28-JUN-2000 07-JUN-2000 07-JUL-2000 07-JUL-2000	17-DEC-2001 (f Genomic sequence Human; oxidored ligase; hyperpp autoimmune diso inflammatory di blood-related d anti arthritic; Homo sapiens. W0200155301-A2. 02-AUG-2001.
000000000000000000000000000000000000000		: 2000US-0217487. 2000US-0218990. 2000US-0220963. 2000US-0224518. 2000US-0224518. 2000US-0225214. 2000US-0225266. 2000US-0252568. 2000US-025568. 2000US-0255757.	20000 20000 20000 20000 20000 20000 20000 20000	2001 (first entry) c.c. sequence #239 encoding novel human enzyme polypeptide. oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; properproliferative disorder; immunodeficiency disorder; mune disorder; neurological disorder; metabolic disorder; matory disorder; cardiovascular disorder; reproductive disorder; related disorder; infectious disorder; gene therapy; cytostatic; rthritic; nephrotropic; anticoagulant; ds. 55301-A2. -2001; 2001WO-US01239.
17-NOV 17-NOV 17-NOV 17-NOV 17-NOV 17-NOV 17-NOV 17-NOV 01-DEC 01-DEC 05-DEC	08-NOV 08-NOV 08-NOV 17-NOV 17-NOV 17-NOV 17-NOV 17-NOV 17-NOV 17-NOV 17-NOV	20 - OC: 20 - OC: 01 - NOI 08 - NOI	13-00 20-00 13-00 20-00 20-00 20-00 20-00 20-00 20-00 20-00 20-00 20-00	PR 14-SEP-2 PR 14-SEP-2 PR 14-SEP-2 PR 14-SEP-2 PR 14-SEP-2 PR 14-SEP-2 PR 21-SEP-2 PR 25-SEP-2 PR 25-SEP-2 PR 27-SEP-2 PR 27-SEP-2 PR 29-SEP-2
2000US -02492 2000US -02492 2000US -02492 2000US -02492 2000US -02492 2000US -02492 2000US -02492 2000US -02492 2000US -02492 2000US -025014	2000US-02466 2000US-02466 2000US-02492 2000US-02492 2000US-02492 2000US-02492 2000US-02492 2000US-02492 2000US-02492 2000US-02492 2000US-02492	2000US-0241 2000US-0241 2000US-0246	2000US-0237 2000US-0237 2000US-0237 2000US-0237 2000US-0237 2000US-0237 2000US-0240 2000US-0240 2000US-0241 2000US-0241 2000US-0241 2000US-0241	9P-2000; 2000US-0232398 9P-2000; 2000US-0232401 9P-2000; 2000US-0232401 9P-2000; 2000US-0233401 9P-2000; 2000US-0233063 9P-2000; 2000US-0233063 9P-2000; 2000US-0233065 9P-2000; 2000US-0234223 9P-2000; 2000US-0234223 9P-2000; 2000US-0234997 PP-2000; 2000US-0235834 PP-2000; 2000US-0235834 PP-2000; 2000US-0235836 PP-2000; 2000US-023636367 PP-2000; 2000US-0236368 PP-2000; 2000US-0236368

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RESULT 8
AAX90036/c
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В
                                                                                                                                                                                                                                                                                                                                                                                            Matches
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05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID No 2049; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 2209 BP; 629 A; 412 C; 442 G; 726 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
15-JUL-1999
                                                                                              Fervidobacterium pennavorans; Ven 5; thermostable pullulanase; pulA; industrial saccharification; ss.
                                                                                                                                             Fervidobacterium pennavorans Ven 5 thermostable pullulanase DNA.
                                                                                                                                                                               17-SEP-1999
                                                                                                                                                                                                              AAX90036;
                                                                                                                                                                                                                                             AAX90036 standard; DNA; 2601 BP
                                W09935274-A2
                                                               Fervidobacterium pennavorans
                                                                                                                                                                                                                                                                                                                            1 GCTTTCTTTGCCAAGAGCG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                      Match 72.5%; Score 17.4; DB 22; Local Similarity 94.7%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                             18;
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2000US-0251719.

2000US-0251479.

2000US-0251856.

2000US-0251868.

2000US-0251869.

2000US-0251989.

2000US-0251989.
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                 (first entry)
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RESULT 9
AAK84218/c
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 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding Fervidobacterium sp. Ven 5 thermostable pullulanase, useful for industrial saccharification processes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVO ) NOVO-NORDISK AS
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                                                                             19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2601 BP; 881 A; 494 C; 596 G; 630 T; 0 other;
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                                                                                                                                           04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 40-41; 52pp; English.
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39030.
                                                                                                                                                                                                                                                                                                                                                                                       AAK84218 standard; DNA; 36135 BP
                                                                                                                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                  AAK84218;
                                                                                                                                                                                                                17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                                                                                                       WO200157182-A2.
                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                            31-JAN-2000;
                                                  11-JUL-2000;
                                                             11-JUL-2000;
                                                                      07-JUL-2000;
                                                                                                                                  18-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TTTCTTTGCCAAGAGCGCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jorgensen PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                       2000US-0189874
2000US-0198123
2000US-0198123
2000US-0205515
2000US-0209467
2000US-0215135
2000US-0216647
2000US-0217688
2000US-0217487
2000US-0217489
2000US-0217489
2000US-0217496
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                         2000US-0180628.
2000US-0184664.
                                                                                                                                                                 2000US-0186350.
                                                                                                                                                                                              2000US-0179065
                    2000US-0220963.
2000US-0220964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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0;

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2000US-0235834
2000US-0235836
2000US-0236327
2000US-0236367
2000US-0236368
2000US-0236369
2000US-0236370
2000US-0236370
2000US-0237038
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2000US-0237038
2000US-0237039
2000US-0237039
2000US-0239337
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2000US-0231414
2000US-0232080
2000US-0232081
2000US-02321968
2000US-02321968
2000US-0232397
2000US-0232397
2000US-0232399
2000US-0232400
2000US-0232401
2000US-0232401
2000US-023401
2000US-023401
2000US-023401
2000US-023401
2000US-023403
2000US-023403
2000US-023423
2000US-023423
2000US-023423
2000US-023423
2000US-0234234
2000US-0234234
                          RATE RATE REPORTED TO A REPORT OF THE REPORT
ARS4951 to AAK64702 encode the human immune/haematopoletic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome cs supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting cc protein. (I) proteins and polynucleotides may be used to prevent, CC cancers and cancer metastases of haematopoletic-derived cells. AAK64703 cc sequences from the present inmune/haematopoletic-derived cells. AAK64703 cc represent sequences used in the exemplification of the present invention.
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17-NOV-2000
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ids encoding human immune/hematopoietic antigen polypeptides,
preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 39030; 3071pp + Sequence Listing; English.
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2000US-0254097.
2001US-0259678.
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2000US-0246524
2000US-0246526
2000US-0246526
2000US-0246532
2000US-0246603
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0249207
2000US-0249207
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249212
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2000US-0249214
2000US-0249215
2000US-0249216
2000US-0249216
2000US-0249218
2000US-0249284
2000US-0249284
2000US-0249284
2000US-0249288
2000US-0249288
2000US-0251988
2000US-0251868
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22-AUG-2000 22-AUG-2000 23-AUG-2000 30-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000

18-AUG-2000; 22-AUG-2000;

14-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-CCT-2000 20-CCT

2000US-0240960.
2000US-0241785.
2000US-0241786.
2000US-0241786.
2000US-0241809.
2000US-0241809.
2000US-02446174.
2000US-02446174.
2000US-0246474.
2000US-0246475.
2000US-0246477.

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RESULT 10
ABV12459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
Matches
                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36135 BP; 10321 A; 8075 C; 8063 G; 9676 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV12459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABV12459 standard; cDNA; 467 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate expression marker cDNA 12450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmacogenomic marker; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2002
                                                                                                                                                                                                              The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                  Claim 1; Page 2053; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        920 CTTTCTTTGCCAAGAGC 904
                                                      Sequence 467 BP; 71 A; 115 C; 132 G; 149 T; 0 other;
                                                                                    patient;(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                              (e) selecting a composition for inhibiting prostate cancer in a patient;(f) assessing the prostate cell carcinogenic potential of a compound;(g) determining whether prostate cancer has metastasized in a patient;(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                       (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                 cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate cancer; cytostatic; carcinogen; pharmacodyanamic
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-183319P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.8%;
               70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17; DB 22; Pred. No. 3.5e+0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
   0;
                            Score 16.8; DB 23;
               Pred. No.
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.5e+02;
                  2.1e+02;
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                               Length 467;
       Indels
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       Gaps
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Db δÃ

376 GCTTTCTTTGGCAAAAGCGC 395

1 GCTTTCTTTGCCAAGAGCGC 20

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Matches
                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-2000; 2000US-183319P.
16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human: prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate expression marker cDNA 33590.
                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                       Claim 1; Page 7105; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 GCTTTCTTTGGCAAAAGCGC
                                                      sequence 506 BP; 80 A; 129 C; 145 G; 152 T; 0 other;
                                                                                                                                                                        (d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
                                                                                                                                                                                                         cancer in a patient;
                                                                                    (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                   patient;
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            Local Similarity
                                                                                                                selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                     detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTTTCTTTGCCAAGAGCGC
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; cDNA;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Endege WO,
                 90.0%;
                             70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monahan JE;
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 0;
                             Score 16.8; DB 23; Length 506;
               Pred. No. 2.1e+02;
   Mismatches
      Indels
      0,
       Gaps
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CC global changes in gene expression in tissues or cells exposed to the CC toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic ceftet of a compound or progression of a toxic effect, preferably the CC expression in a tissue or cell sample exposed to the compound of the compound of the compound of the compound of two or CC more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. CC the method can also be used to identify an agent which modulates the compount in kit form), where each of the probes computed that system comprising at database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a system comprising at least two genes listed in the specification. The method is user interface to view the information used to present information cc listed in the specification. The method is useful for elucidating global cc listues or cell expression and for identifying to present information used to present information cc tissues or cell exposed to a hepatotoxin of a compuse or cell exposed to a hepatotoxin of a compuse in gene expression level in a tissue or cell of at least one gene changes in gene expression and for identifying toxicity markers in cc sample that has been exposed to a hepatotoxicity markers in drug screening and toxicity assays. The genes and cc gene expression information may be used as diagnostic markers for the scalar ctrised by centrilobular necrosis and steatosis. The present cc sequence is an expressed sequence tag (EST) or cDNA derived from a gene
            The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Seq ID No 1639; 239pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-241625/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mendrick D, Porter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JuL-2001; 2001WO-US23872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200210453-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat sequence differentially expressed in response to a hepatotoxin #1639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK63732 standard; cDNA; 1679 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-2002
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2001US-290645p
2001US-292336p
2001US-295798p
2001US-297457p
2001US-298884p
2001US-303459p
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expressed sequence tag (EST) or cDNA derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          centrilobular necrosis; steatosis
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                                                       Matches
                                                                                Query Match
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                                                                                                  Sequence 2304 BP; 541 A; 640 C; 721 G; 402 T; 0 other;
                                                                                                                                                                   useful in developmental biology and in elucidating cell signalling cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 3455; 21pp + Sequence Listing; English.
    226
                                                                                                                                                                                                                                                                                                                                  genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABB58888
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster expressed polynucleotide SEQ ID NO 3455.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which is differentially expressed in response to a hepatotoxic agent.
                         4 TTCTTTGCCAAGAGCGCCGC 23
                                                                    TOCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TCTTTGCCTTGAGCGCCGCA 80
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TTCTTTGCCCAGAGCGCAGC 245
                                                       18;
                                                                  Similarity
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                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                           70.0%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Li PWD,
                                                                                                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
                                                                        Score 16.8; DB 23; Length 2304;
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                                                   Mismatches
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                                                           No.
                                                          2.7e+02;
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                                                 Indels
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                                              0;
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RESULT 14
ABL02990
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                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL018176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-ABB72072).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3452; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical; gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                       sequence 4446 BP; 1191 A; 1023 C; 1084 G; 1148 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions -
altered culture condition; environmental stress; physiological provocation; ds.
                             Differential gene expression; genomic sequenced tag; GST;
                                                         Bacillus clausii genomic sequence tag (GST) #3572.
                                                                                                                                                 ABK80729 standard; DNA; 408 BP
                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                          13-AUG-2002
                                                                                                                                                                                                                         613 TTCTTTGCCCAGAGCGCAGC 632
                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                        4 TTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M,
                                                                                                                                                                                                                                                                                  Conservative
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                70.0%; Score 16.8; 90.0%; Pred. No. 3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li PWD,
                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers EW;
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                  3e+02;
                                                                                                                                                                                                                                                                                                                   DB 23; Length 4446;
                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                          0;
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Search completed: March 17, 2003, 10:50:45

time

: 146.715 secs

g

374 GCATTCTTGCCCAAGTGCGCCGC 396

Gaps

0

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The invention describes a method of monitoring differential expression of compens in a first Bacillus cell relative to expression of the genes in cother Bacillus cells, comprising hybridising labelled nucleic acid probes content to the genes in a first Bacillus cells to a substrate containing array of Bacillus cell sequenced tags (GST), examining the array, and determining compension by an observed hybridisation reporter signal of compension of the array of Bacillus cell relative to expression of the same genes comes in a first Bacillus cell relative to expression of the same genes compension of several genes from a Bacillus cell, discovering new compension of several genes from a Bacillus cell, discovering new compension of several genes from a Bacillus cell, discovering new compension of several genes from a Bacillus cell, discovering new compension of several genes from a Bacillus cell, discovering new compension of several genes from a Bacillus cell, discovering new compension of genes may be used to provide a representation of the way in expression of genes may be used to provide a representation of the way considered the sequence of compension of the same to changes in culture conditions, considered the sequence of the sequence of the sequence of the sequence represents a genomic sequence information is considered to the sequence of the sequence represents a genomic sequence tag (GST) used in the sequence represents a genomic sequence tag (GST) used in
QV
                                           Matches
                                                                                    Query Match
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27-MAR-2001; 2001US-279526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-OCT-2001; 2001WO-US31437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200229113-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus clausii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID NO 8020; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequenced tag array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus cells, by using substrate containing Bacillus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO)
                                                                                                                                                                                                              the method of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVOZYMES BIOTECH INC
                                                                                                                           Sequence 408 BP; 106 A; 86 C; 104 G; 111 T; 1 other;
                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                  Local
  1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVOZYMES
                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clausen IG;
                                                Conservative
                                                                69.2%; Score 16.6; DB 24
82.6%; Pred. No. 2.5e+02;
                                                  0;
                                                    Mismatches
                                                                                           DB 24; Length 408;
                                                      4;
                                                      Indels
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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                             Database :
  US-09-836-439-3
24
1 gctttctttgccaagagcgccgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                            16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      March 17, 2003, 10:23:12; Search time 848.387 Seconds (without alignments) 458.154 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                    gb_est1: *
gb_est2: *
gb_htc: *
gb_est3: *
gb_est4: *
gb_est5: *
                                                                                                                                                                                                                              em_estro:*
em_htc:*
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em_gss_mus:*
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em_gss_rod:*
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em_gss_inv:*
em_gss_pin:*
em_gss_vrt:*
em_gss_fun:*
                                               em_gss_mam:*
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gb_gss:*
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639637 hel	3963	14	606	9.	21.4	45
638554 hd24h07.	385	14	606	٥	۲.	44
12251 DKF2	225	9	605	9	۲	43
2638120 hd18g02.	381	14	604	9	۳.	42
636906 he03a11.	3690	14	599	9	۲.	41
38291 hd20g07.	382	14	595	9	21.4	40
11507 DKFZp686D	150	9	591	9	-	39
Q640394 he27h1	4039	14	590	9.	۲	38
07a10.	BQ637208	14	587	9	21.4	37
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88176 UI-E-C	8817	14	578	9	1.	35
85757 UI-E-C	68575	14	578	9	-	34
04430 UI-E-CI1	70443	14	576	9		ω ω
40490 he	049	14	575	9	21.4	32
Q636602 hdllh09.	63660	14	562	9		31
Q639356 he14e06.	63935	14	549	9.	1.	30
36918 he03c02.	63691	14	549	9	1.	29
40241 he26a01.	64024	14	535	9.	1.	28
38268 hd20e05.	63826	14	530	9	21.4	27
38124 hd18g07.	63812	14	530	9.	21.4	26
90115 UI-E-CLC	9011	14	530	9.	<u>, </u>	25
9829 he	BQ639829	14	526	9.		24
40660 he31f02.	4066	14	514	9.		23
90319 UI		14	513	9.	-	22
37734 he13h0	3773	14	510	9	-	21
877 EST19137 H	877	14	505	9	_	20
86188 UI-E-CI	36		504	9	_	19
Q636862 he02e01.	Q63686	14	503	9	_	18
40665 he31f09.	064066	14	499	9	۳,	17
M690311 UI-E-C	69031	14	496	9	۳	16
M691592 UI-E-C	M69159	14	493	9		5
90137 UI-E-C	M69013	14	493	9	<u>'</u>	14
M662914 UI-E-C	M66291		478	9		3
M688069 UI-E-C	M6880		474	9	-	12
Q250368 TaE25	25036	14	471	9		11
712402 DKFZp6	240	9	471	9		10
M688227 UI-E-CL	82	14	469	9	21.4	9
M696193 UI-È-CL	9619	14	446	89.2	21.4	∞ ⋅
412 DKFZp686	41	9	442	9	21.4	7

ALIGNMENTS

	COMMENT	MEDLINE		TITLE	AUTHORS	REFERENCE		OKOMILOM	ORGANISM	KEYWORUS	VERSION	ACCESSION		DEFINITION	LOCUS	BM694379	,
Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoareseblue.weeg.uiowa.edu Tissue Procurement: Dr. Gregg Hageman CIDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa	Contact: Soares, MB	Genome wes. 6 (9), 791-800 (1990) 97044477	discovery	Normalization and subtraction: two approaches to facilitate gene	Bonaldo, M.F., Lennon, G. and Soares, M.B.	1 (bases 1 to 303)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sanions	EST.	BM694379.1 GI:19007637	BM694379	UI-E-CI1-afp-p-18-0-UI 5', mRNA sequence.	-afp-p-18-0-UI.rl UI-E-CIl Homo sapiens cDNA	BM694379 303 bp mRNA linear EST 28-FEB-2002		

Result No.

Score

Match

Length DB

IJ

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

a

89.2 89.2 89.2 89.2

303 14 319 14 337 14 340 14 349 14

BM694379 BQ637565 BM723222 BM682444 BM703950 BM690151

BM694379 UI-E-CI1-BQ637565 hellg04.y BM72322 UI-E-EJ0-BM682444 UII-E-EJ0-BM703950 UI-E-CK1-BM690151 UI-E-CL0-

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ACCESSION
VERSION
                                                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                        Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts work. Vis. 8 (4), (2002) In press
                                                                                                                                                            Email: graeme@helix.nih.gov
Plate: 11 row: g column: (
                                                                                                                                                                                                                 Tel: 301 402 3452 Fax: 301 496 0078
                                                                                                                                                                                                                                                                                               Section on Molecular Structure and Function National Eye Institute
                                                                                                                                                                                                                                                                                                                                                    Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ637565 319 bp mRNA linear EST 15-JUL-2002 hellg04.yl Human Retina cDNA (Un-normalized, unamplified): hd/he Homo sapiens cDNA clone hellg04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
22; Conserv
                                                                                                                                Seq primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 319)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DHIOB (Life Technologies) (TI phage resistant)"
/lab_host="DHIOB (Life Technologies) (TI phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: Ecor I; Site_2: Not I;
UI-E-CII is a normalized cDNA library containing the
following tissue(s): RPE and Choroid. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an Ecor I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is ACCTA.
This library was created for the program, Gene Discovery
in the Visual Suctom approach to the server to the tree to the containts.
/db_xref="taxon:9606"
/clone="hellg04"
                                                     /organism="Homo sapiens"
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in the Visual System, supported by National Eye Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="RPE and Choroid"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="UI-E-CI1-afp-p-18-0-UI"
/clone_lib="UI-E-CI1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.2%;
95.7%;
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                                                                                                                                                               column: 04
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Pred. No. 23
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                             sequence: 295-332, >AT_rich#Low_complexity (matched compliment)
                                                                                                                                                                                                                                                                                                                                         Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM723222 337 bp mRNA linear EST 01 UI-E-EJO-aio-i-15-0-UI.r1 UI-E-EJO Homo sapiens cDNA clone UI-E-EJO-aio-i-15-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 337)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 Eckstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Iowa
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                                                                                                                                                                                                                                                                                                            The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORPT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGTTCGCGAGCGCCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE a
                                                            /clone="UI-E-EJO-aio-i-15-0-UI"
/clone_lib="UI-E-EJO"
                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Human Retina cDNA (Un-normalized, unamplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medical Research Building Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.2%;
95.7%;
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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SOURCE

TITLE

KEYWORDS VERSION RESULT 3 BM723222

Locus

Db

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KEYWORDS
SOURCE
ORGANISM
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BM682444/c
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                                                                                                                                                                                                                                                                                                                                                Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                            Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA sequence: 1-37, >AT_rightLow_complexity (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM682444 340 bp mRNA linear EST 27-UI-E-EUO-aio-1-15-O-UI.sl UI-E-EUO Homo sapiens cDNA clone UI-E-EUO-aio-1-15-O-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loases 1 to 340)
Bonaldo, M.F., Lennor
                                                                                                                                                                                                                       POLYA-Yes.
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                                                                                                                                                                                                                                                   Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Not I;
UI-E-EJO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dTyl8 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCGCCAT; oppic nerve, CCATTAGTG; retina, CCGGG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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                                           /clone="UI-E-EJO-aio-i-15-0-UI"
/clone_lib="UI-E-EJO"
                                                                                                                                                                   1. .340
/tissue_type="fetal eyes, lens, eye anterior segment,
                                                                                                     /db_xref="taxon:9606"
                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                     Location/Qualifiers
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95.7%;
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Pred. No. 24;
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В

Matches

MEDLINE COMMENT

FEATURES

/clone="UI-E-CK1-afk-m-09-0-UI"

COMMENT

JOURNAL TITLE REFERENCE

VERSION KEYWORDS SOURCE

SDOOT

AUTHORS

TITLE JOURNAL

VERSION ACCESSION DEFINITION

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REFERENCE
AUTHORS
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BM703950
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                                                                                                                                                        Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                             Genetics (www.resgen.com).
Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                     Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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349 bp mRNA linear EST 28
UI-E-CK1-afk-m-09-0-UI.rl UI-E-CK1 Homo sapiens cDNA clone
UI-E-CK1-afk-m-09-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG_SEQ=CCGCG"
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/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted cDNA library constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
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95.7%;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM690151 441 bp mRNA linear FUI-E-CLO-acd-f-11-0-UI.rl UI-E-CLO Homo sapiens cDNA UI-E-CLO-acd-f-11-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                         Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
                                                                                                                                                                                                                                                    Genetics (www.resgen.com).
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CLO-clone_11b="UI-E-CLO"
/tlssue_type="human retina"
/dev_stage="adult"
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/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CK1 is a normalized cDNA library containing the
following tissue(s): Retina Foveal and Macular. The
library was constructed according to Bonaldo, Lennon and
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/tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 to 441)
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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95.7%;
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Pred. No. 24;
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FEATURES

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Gaps

COMMENT

MEDLINE JOURNAL REFERENCE

TITLE AUTHORS SOURCE VERSION ACCESSION

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RESULT 7
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          Best Local Similarity
                                   Query Match
                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.)
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKFZp68601888_r1 686 (synonym: h
DKFZp68601888 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 442)
                                                                                                                                                                                                                                                                                                                                                                          Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No s1 sequence available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wambutt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone (DKFZp68601888) is available at the RZPD in Berlin
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                                                                                                              106 a
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                                                                                                                                  /lab_host="DH10B"
/note="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
                                                                                                                                                                                                                                                    /clone_"DKFZp68601888"
/clone_lib="686 (synonym: hlcc3)"
                                                                                                                                                                                                         /tissue_type="human skeletal muscle"
/dev_stage="adult"
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/db_xref="taxon:9606"
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95.7%;
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                 89.2%;
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                 Score
Pred.
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                    No. 26;
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                                          Length 442;
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                                      226 GCGTTCTTTGCCAAGAGCGCCGC 248
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                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                   Similarity
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1 (bases 1 to 446)

Bonaldo, M.F., Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM696393 446 bp mRNA linear EST 28-
UI-E-CL1-afa-d-24-0-UI.rl UI-E-CL1 Homo sapiens cDNA clone
UI-E-CL1-afa-d-24-0-UI 5', mRNA sequence.
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                                                                                                                                          Conservative
                                                                                                                                                                                                                                           //lab_host="DHIOB (Life Technologies) (T1 phage resistant)"
//lab_host="DHIOB (Life Technologies) (T1 phage resistant)"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacla) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CLI is a normalized cDNA library containing the
following tissue(s): retina. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
sequence tag for this library is CCGCG. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."

95 a 148 c 106 g 96 t l others
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/dev_stage="adult"
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/db_xref="taxon:9606"
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95.7%;
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                                                                                                                                                           Score 21.4;
Pred. No. 26;
                                                                                                                                    Mismatches
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82 GCGTTCTTTGCCAAGAGCGCCGC 104
                                                                                                                                                                                           Local Similarity
                                                                       1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence: 425-459, >AT_rich#Low_complexity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 469)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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//DE__SCAPE_C
                                                                                                                                                       Conservative
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/dev_stage="adult"
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/clone_lib="UI-E-CL0"
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                                                                                                                                               0; Mismatches
                                                                                                                                                                                       Score 21.4;
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Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKFZp686N1788_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686N1788 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.viemann@dkfz-heidelberg.de; sequenced by AGOWA_(Berlin/Germany) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone (DKFZp686N1788) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405. Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TaE25006AllR TaE25 Triticum aestivum cDNA clone TaE25006AllR, mRNA
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was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
                                                                                                 Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                                                                                              Unpublished (2002)
Contact: Dr. Sylvie Cloutier
                                                                                                                                                                                                                                                                                                            Triticum aestivum
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                                             Email: scloutier@em.agr.ca
                                                                                                                                                                                     Wheat functional genomics - Glenlea developing seeds cDNA libraries
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                                                            (204) 983-2340
(204) 983-4604
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/dev_stage="adult"
/lab_host="BH10B"
/note="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
158 c 99 g 105 t
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/clone_lib="686 (synonym: hlcc3)"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Average insert size is >870 bp plate: 006 row: A column: 11 Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM688069 474 bp mRNA linear EST 28 UI-E-CLO-abv-c-04-0-UI.rl UI-E-CLO Homo saplens cDNA clone UI-E-CLO-abv-c-04-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                              Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 335-367, >AT_rich#Low_complexity
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome_Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
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Site_1: NotI, Site_2: MiuI; mRNA obtained from wheat seeds
of cultivar Glenlea 25 days post-anthesis"
a 164 c 108 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="developing seeds"
/dev_stage="25 days after anthesis"
/lab_host="E. coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="TaE25006A11R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="Glenlea"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .47
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/lab_host-"DH10B (Life Technologies) (T1 phage resistant)" /note-"Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                                                                                                                               /organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="UI-E-CLO-abv-c-04-0-UI"
/clone_1ib="UI-E-CLO"
                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                           /dev_stage="adult"
                                                                                                      /tissue_type="human retina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 to 474)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.2%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 28-FEB-2002
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Query Match
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Forward POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 478)

Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM662914 478 bp mRNA linear EUI-E-CKO-aan-e-04-0-UI.Sl UI-E-CKO Homo sapiens cDNA UI-E-CKO-aan-e-04-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Res. 6 (9), 791-806 (1996)
/lab_host-"DHIUB (Life Technologies) (Tl phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UT-E-CRO is a cDNA library containing the following
tissue(s): Retina Foveal and Macular. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
                                                                                                                                                                                                                                                                                                      /organism-"Homo sapiens"
/db_xxef-"taxon:9606"
/clone="UI-E-CKO-aan-e-04-0-UI"
/clone_Lib-"UI-E-CKO"
                                                                                                                                                                                                                                                                     /tissue_type="Retina Foveal and Macular"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Pred. No. 27;
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REFERENCE

TITLE

SOURCE KEYWORDS VERSION ACCESSION DEFINITION

ORGANISM

RESULT 13 BM662914/c

ORIGIN BASE COUNT

COMMENT

COMMENT

MEDLINE JOURNAL TITLE AUTHORS

REFERENCE

KEYWORDS VERSION ACCESSION BM690137 RESULT 14 ORIGIN

Matches

JOURNAL MEDLINE

FEATURES

source

FEATURES

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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                sequence: 425-459, >AT_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM690137 493 bp mRNA linear EST 28.
UI-E-CLU-acd-d-08-0-UI.rl UI-E-CLU Homo sapiens cDNA clone
UI-E-CLU-acd-d-08-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
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1 (bases 1 to 493)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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/tissue_type="human retina"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DHIOB (Life Technologies) (T1 phage resistant)"
/note="organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UT-E-CLO is a cDNA library containing the following
tissue(s): retina. The library was constructed according
to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="UI-E-CLO-acd-d-08-0-UI"
/clone_lib="UI-E-CLO"
                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_LIB-UI-E-CKO
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                                                                                                                                                                                                                                                                                                                                                             . 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.7%;
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493 bp mRNA linear EST 28
UI-E-CI1-abh-c-07-0-UI.rl UI-E-CI1 Homo sapiens cDNA clone
UI-E-CI1-abh-c-07-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 493)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 302-335, >AT_rich#Low_complexity
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hayeman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
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Tel: 319 335 8250
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/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/lab_host="DH10B (Life Technologies
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95.7%; Pred. No. 27;
tive 0; Mismatches
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COMMENT

MEDLINE JOURNAL

FEATURES

source

REFERENCE

AUTHORS

TITLE

SOURCE KEYWORDS VERSION ACCESSION

ORGANISM

adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)

BASE COUNT 116 a 157 c 111 g 109 t

Matches Query Match Best Local Similarity Conservative 89.2%; 95.7%; 0; Score 21.4; Pred. No. 27; Mismatches Indels 0; Gaps 0,

DB 14;

Length 493;

밁 8 GCGTTCTTTGCCAAGAGCGCCGC 30 1 GCTTTCTTTGCCAAGAGCGCCGC 23

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Matches

DEFINITION BM691592

Focus RESULT 15 BASE COUNT

Search completed: March 17, 2003, 13:09:15 Job time: 851.387 secs

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Minimum I
Maximum I
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  IDENTITY_NUC Gapext 1.0
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22
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Listing first 45 summaries
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Pred. ŏ. S the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result ĕ Score 20 20 20 20 19 19 19 19 Match Length Query 1798795 1198795 1186638 185841 2018461 201849 2052 2052 2209 2411 37808 41578 63484 63484 63484 63484 63484 113632 113632 113955 113977 12072 12072 120 133095 DB SCYPL252C SC39KCX91 SC39KCX91 CBRG46G14 AC109155 AC139156 AC13126B AC13126B AC131317 AC1092031 AL13917 AC095684 AC095684 AC004841 AC095684 AC0111035 AC019125 AC111035 AC019125 AC093799 AC093799 AC093799 AC093799 AC093799 AC093799 AC093799 AC09379 AC093799 AC09379 AC093623 AP005572 AC117913 AC113320 AC069223 AC068763 AC027080 AC027080 AC130437 AC022912 AC046146 AC095531 AF012746 AL139147 Human DNA AC092031 Homo sapi AL137158 Homo sapi AC168291 Homo sapi AC068291 Homo sapi AC095684 Rattus no AP005487 Oryza sapi AC004841 Homo sapi AF112374 Danio rer AL845428 Danio rer AL845428 Danio rer AL845428 Danio sapi AC019195 Homo sapi AC019195 Homo sapi AC068389 Homo sapi AC091216 Caenorhab AC109155 Mus muscu AC109155 Mus muscu AC108916 Mus muscu AC131268 Homo sapi AC119622 Rattus no AC069223 Homo sapi AC069763 Homo sapi AC027080 Homo sapi AC130437 Homo sapi AC022912 Homo sapi AC023623 Homo sapi AC05572 Oryza sat AF012746 Danio rer Z73608 S. cerevisia AC046146 Description S.cerevisia S.cerevisia S.cerevisia Caenorhab 20 Mus muscu 4 Human DNA 0 Homo sapi 9 Homo sapi 5 Rattus no 5 Homo sapi 6 Rattus no 0 Rattus no 0 Rattus no 0 Partus no 0 Partus no 0 Homo sapi 9 Oryza sapi 1 Oryza sapi 1 Oryza sapi 1 Oryza sapi 1 Oryza sapi Human Rattus no Mus muscu

KEYWORDS SOURCE ORGANISM RESULT 1 AC046146 LOCUS REFERENCE VERSION ACCESSION DEFINITION AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 13095)
Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., AC046146 AC046146.6 GI:16118085 HTG; HTGS_PHASE1. Mus musculus. ACO46146

133095 bp DNA linear HTG 16-OCT-2001
MUS musculus chromosome 12 clone RP23-321N21, *** SEQUENCING IN
PROGRESS ***, 31 unordered pieces.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted (13-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 14, 2001 this sequence version replaced gi:11094634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K. and Gibbs, R. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project Information
Center project name: MADV
Center Clone name: RP23-321N21
Center Clone name: RP23-321N21
Sequencing vector: M13; LO8821
Sequencing vector: M13; LO8821
Sequencing vector: M13; LO8821
Chemistry: Dye-terminator Big Dye: 6% of reads
Chemistry: Dye-terminator Big Dye: 6% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 118378 bases at least Q40
Consensus quality: 144876 bases at least Q30
Consensus quality: 155160 bases at least Q20
Estimated insert size: 148882; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 2.1x in Q20 bases; sum-of-contigs estimation
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COMMENT

TITLE

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RESULT 2
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          REFERENCE
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                                                                       KEYWORDS
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Best Local
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 AUTHORS
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                                                                                                                                                                                                                                 Local Similarity
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                                                  Rattus norvegicus
                                                                                           AC095531
                                                                                                   Rattus norvegicus clone CH230-8N2, 58 unordered pieces.
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                         HTG; HTGS_PHASE1.
                                                                                   AC095531.3 GI:21716992
                                                                                                                           AC095531
                     Rattus.
                                                               Norway
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         (bases 1 to 152147)
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30809 c 29300 g
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/chromosome="12"
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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126536: contig
126636: gap of
130483: contig
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97229: contig o
97329: gap of u
100516: contig o
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118929: gap of
121281: contig
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95.5%;
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107955: contig
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123762: contig
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                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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SEQUENCING IN PROGRESS ***,
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* consists of 58 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence

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Alsbrocks S.L., Ammarthungs, H.C., Are, J.R., Ayele, M., Banks, T., Batbaria, J., Benton, J., Bindge, K., Blankenduy, K. Bontin, D., Bouck, J., Benton, J., Bindge, K., Blankenduy, K., Bontin, D., Burch, J., Bryant, K.P., Edward, S., Bronn, M., Bryant, N.P., Charco, J., Gener, M., Cavazos, S.R., Chacko, J., Chavez, D., Chlen, G., Chen, K., Chen, Z., Chowdry, J., Chlen, G., Chen, J., Gener, H., Dignan, Bocch, S., Tunthin, K.J., Bernhart, C.D., Good, J., Gerctia, A., Garner, T., Garza, M., Gill, R., Gorrell, J.H., Guevara, M., Gunarathne, J., Hakes, A., Henrandez, J., Herris, K., Horder, J., Hully, S., Humb, J., Jackson, L.E., Bernhart, C., Georgia, H., Gorrell, J.H., Guevara, M., Gunarathne, J., Hakes, A., Henrandez, J., Herris, K., Horder, M., Hully, S., Humb, J., Jackson, L.E., Bernhart, C., Horder, M., Luck, P., Hakes, A., Herris, M., Horder, M., Hully, S., Humb, J., Jackson, L.E., Bernhart, C., Hakes, A., Herris, K., Horder, M., Lucker, R., Luna, R., Martinez, J., Kerlovit, J., Khang, R., Hart, M., Hully, S., Humb, J., Jackson, L.E., Reitz, G., Hull, J., J., Hull, M., Loulseged, H., Lucker, M., Lucker, R., Luna, R., Martinez, J., Kerlovit, J., Khang, R., Hart, M., Hully, S., Stanley, H., Stone, H., Hart, J., Hully, S., Humb, J., Jackson, L.E., Reitz, G., Hull, J., Luna, R., Martinez, J., Kerlovit, J., Hull, J., Luna, R., Martinez, J., Hull, J., Luna, R., Martinez, J., Kerlovit, J., Huller, J., H
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

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as soon as it is available and the accession number will be preserved.
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RESULT 3
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ORGANISM
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C. Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Blimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P. Bunket,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,Z., Chowdhry,L., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
                                                                                                                                                                                        AC117913 172497 bp DNA linear HTG 18-JUL-
Rattus norvegicus clone CH230-35D24, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                             21;
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                            Rattus norvegicus
                                                                                                                                                           AC117913.4 GI:21747159
                                                                                              Rattus
                                                                                                                                    Norway rat.
                                                                                                                                                HTG; HTGS_PHASE1.
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Hemsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Maheshwari,M., Meidor,M., Meidor,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogah,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Partmus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,L., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Thomas,N., Thomas,S.,
Ward-Moore,S., Warren,R., Washington,C., Watliamson,A., Wilczyk,R., Wooden,S., Watliamson,A., Wilczyk,R., Wooden,S., Watliamson,A., Wilczyk,R., Wooden,S., Watliamson,A., Wilczyk,R., Wooden,S., Watliamson,S.,
Wu,Y., Wu,Y., Wu,Y., Wu,Y., Wu,Y., Shou,J., Zorriila,S., Nelson,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Belaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franchici, T., Ferraguto, D., Flagg, N., Ford, J., Flagg, N., 
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Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
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NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/eenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 59 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 118901 bases at least Q40
Consensus quality: 125278 bases at least Q30
Consensus quality: 129335 bases at least Q20
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------ Project Information
Center project name: GVPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor C
Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
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AC113320
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Best Local (
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E 2 (bases 1 to 188795)

E 2 (bases 1 to 188795)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastlen,V., Boguslavkiy,L., Boukhgalter,B.,
Anderson,S., Barna,N., Bastlen,V., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Camaratta,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferrefira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Plerre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczky,J., Levine,R., Liu,G., MacLean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 188795)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, Clone RP23-445E16
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                     AC113320.2 GI:22474991
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
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Gaps

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REFERENCE AUTHORS

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RS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkly, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacClean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Tembek, L., Zimmer, A. and Zody, M.
Direct Submission
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Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                  * consists of 11 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                           by the finished sequence the accession number will be preserved.

1 47353: contig of 47353 bp in length
47354 47453: gap of 100 bp
47454 48767: contig of 1314 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 185500 bases at least Q40 Consensus quality: 18954 bases at least Q30 Consensus quality: 187365 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L22784
Center clone name: 445_E_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 9.1 in Q20 bases; agarose-fp Quality coverage: 9.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
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Insert size: 187795; sum-of-contigs
                                                                                                                                                                                                                                                                            the finished sequence as soon as it is available and
         48768 48867: gap of 48868 50642: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www-seq.wi.mit.edu
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ρ of 100 bp
contig of 1775 bp in length
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COMMENT

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Db 36223 AAGAAAAAATCTAGACAAACAA 36244
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                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                      179767 bp
Homo sapiens 3 BAC RP11-398021 (
BAC Library) complete services
ACO60277
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 179767)
                                                                  Homo sapiens.
                                                                                                 AC069223.15 GI:13489121
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60913 6276
62766 62865:
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52086 545
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96248 188795: contig of 92548 bp in length
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72530 72629:
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50743 5191
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96248 .188795
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48868. .50642
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l. .47353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                  92.7%; Score 20.4; I
95.5%; Pred. No. 61;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                742: gap of 100 bp
100 bp 11243 bp in length
105: gap of 100 bp
105: gap of 2443 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58116: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216: gap of 100 bp
60812: contig of 2596 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12: gap of 100 bp 62765: contig of 1853 l
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contig of 23518 bp in length
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                                                                                                                                                 p DNA linear PRI 30-MAR-2001 (Roswell Park Cancer Institute Human
                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 188795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Benton, J., Blankesburg, K., Banks, T., Barks, C., Burch, S., Brieva, M., Bryant, N.P., Buky, C., Burch, P., Burkett, C., Burchl, K.L., Byrd, N.C., Carron, T.F., Chen, G., Chen, C., Chen, G., C
                                  Direct Submission
                                                                          Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 179767)
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COMMENT Submitted (30-MAR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 30, 2001 this sequence version replaced gi:13430920. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email Submitted (22-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 179767)

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

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STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,

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Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons

flanked by consensus splice sites that maintained continuity across the splice junctions. Sequences identical matches are annotated as similar Sequences that are not

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for annotation as Low Coverage. a region does not meet this standard, it will be indicated in the

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

QUALSTAT-REPORT-----

5 10 15 20	1000 900 900 800 500 400 400 100 0 * * * *	Distribution of Quality < 40	Position Original+Context 3 atccaaanaa(n)tctgatcttc 107934 agcctcttttn(n)acagagact 107935 gcctcttttn(n)acagagacta 159144 atggcaatca(n)cacacatggt	Contig length: Phrap values in estimate: Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40 : Number of consensus changing edits: Number of N's in consensus :
25	•	0 Bases	dits a a a	e
30	* *	es •	Edit tccg igcct igcctc	
35	* * * * * *		Edited+Context tccgcpaa(t)tc gcctcttt(t)ta cctcttttt(t)ac tggcaatca(c)ca	144040
40			Edited+Context atccgcggaa(t))ctgatcttc agcctctttt(t)tacagagact gcctcttttt(t)acagagacta gcgcaatca(c)cacacatggt	179767 179551 4.4907e-06 0.00499023

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Phrap Value Range

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Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Bileva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.E., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
                                                                                                                      Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                        BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                        Homo sapiens 3 BAC RP11-133K20 (Roswell Park Cancer Institute Human
                                                                                                                                                                                                                                                                                                                                                 AC068763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                  AC068763.11 GI:14669935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name="G21620"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Region similar to Homo sapiens mRNA; cDNA
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complement/1000
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95.2%;
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REFERENCE AUTHORS

JOURNAL TITLE

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Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
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Mulczyk,R., Wooden,S., Marton,S., Land Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                Submitted (02-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-JUL-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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                                                                              Submitted (25-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 11, 2001 this sequence version replaced gi:13493008.
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Baylor Plaza, Houston,
4 (bases 1 to 180638)
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gc-help@bcm.tmc.edu
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                                           INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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COMMENT

REFERENCE

JOURNAL TITLE AUTHORS

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Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT-----

Contig length: Phrap values in estimate: Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40: Number of consensus changing edits: Number of N's in consensus:	Summary Statistics
180638 1.79362 1.00944e-05 0.00994637 49	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

109869 109872 113503 113504 1135301 125301 73566 73567 73596 73704 73721 73721 73722 73722 73722 73748 73750 73796 73796 ctgtaagctt(n)ttaacactca ttttttttt(g)gagagatct gtgggaggga(n)ganggggtgg ggagganga(n)ggggtggga gttgcctcca(n)accattttaa ttgcctccan(n)ccattttaac agatogogoc(a)cogcactoca atctcagotc(n)ctgcaacttc tcaggagatt(n)tcctgcctca tcctgcctca(n)ctcccaaat tcctgcctca(n)ntgggattac tcccaaata(n)ntgggattac tcccaaatan(n)tgggattac tcccaactac(n)ggctaatttt gtgttgggat(n)acaggcgtga gtgagccacc(n)ngcctggcct ctgataattc(n)gcttttttc
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RESULT 7 ACO27080 LOCUS DEFINITION ACCESSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS AUTHORS	Query Match Amest Local Matches 2 Qy 1 AAG Qy 1 H Db 163480 AAG	7	
AC027080 Homo sapiens chegouence, 22 ur AC027080.2 GI: AC027080.2 GI: HTG: HTGS_PHASE Homo sapiens. Homo sapiens Eukaryota; Meta Mammalia; Euthel (bases 1 to Birren, B., Linth Homo sapiens chopublished (bases 1 to Birren, B., Linth Homo sapiens chopublished (collymore, A., Compopiano, A., Collymore, A., Collymore, A., Condagan, J., Garand-pierre, N. Klein, J., Larock Kl	h Similari 20; Cons GAAAAAATC	1000 900 900 800 600 500 400 300 200 100 0	137774 141481 151926 180507 180509 180510 180511 180511 180513 180514 180514 180515 180516 180515
185841 bp DNA linear HTG 19-APR-2000 ans chromosome 3 clone RP11-548023 map 3, WORKING DRAFT 22 unordered pieces. 18 GI:7596901 PHASEI; HTGS_DRAFT. 28 GI:7596901 PHASEI; HTGS_DRAFT. 29 SI:7596901 PHASEI; HTGS_DRAFT. 20 SI:7596901 PHASEI; HTGS_DRAFT. 20 SI:7596901 PHASEI; HTGS_DRAFT. 21 Lo 185841) Linton,L., Nusbaum,C. and Lander,E. 22 Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., 23 July Silver,B., Brown,A., Burkett,G., 24 Lo 185841) Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., 25 July Silver,B., Brown,A., Burkett,G., 26 July Silver,B., Brown,A., Burkett,G., 27 July Barna,N., Bastien,V., Beda,F., 28 July Silver,B., Brown,A., Burkett,G., 29 July Silver,B., Brown,A., Burkett,G., 20 July Silver,B., S	Location/Qualifiers 88.2%; Score 19.4; DB 9; Length 180638; ty 95.2%; Pred. No. 1.6e+02; ervative 0; Mismatches 1; Indels 0; Gaps 0; TAGACAAGCA 21	* 5 10 Ph	ctaggngtg(n)gcctcacgcc tagcacaatg(n)actttaagct atactcagaa(n)aaatccaaa tcaccaggtg(n)gnnnnnnntat ccaggtgngn(n)nnnnnntatg caggtgngnn(n)nnnnntatgg aggtgngnnnn(n)nnntatggtaa tggngnnnnn(n)nntatggtaa tggngnnnnn(n)ntatggtaa tggngnnnnn(n)ntatggtaa tggngnnnnn(n)ntatggtaa tggngnnnnn(n)ntatggtaa tggngnnnnn(n)naaaaaatttt ttgtaattca(n)aaaaaatttt Distribution of Quality < 40 Bases

TITLE JOURNAL COMMENT

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Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Stojanovic, N., Subramanian, A., Talamas, J., Tesafaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Nipper Sainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (26-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 19, 2000 this sequence version replaced gi:7329443. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 4.0 in Q20 bases; agarose-fp Quality coverage: 4.1 in Q20 bases; sum-of-contigs
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Consensus quality: 172210 bases at least Q40
Consensus quality: 178990 bases at least Q30
Consensus quality: 178990 bases at least Q20
Consensus quality: 181814 bases at least Q20
Insert size: 18900: agarose-fp
Insert size: 183741; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                       51039: gap of 100 bp
61135: contig of 10096 bp in length
61255: gap of 100 bp
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69882: gap of
77230: con
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69782: contig of 8547 bp in length
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77331 86536: contig of 9206 bp in length
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TITLE
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                                                                                                                                                                                                                                                                  Nammalla: Eutheria: Primates; Caraniata; Vertebrata; Euteleostomi; Mammalla: Eutheria: Primates; Catarrhini; Hominidae: Homo.

ICE 1 (bases 1 to 201416)

RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Arej, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burel, R., Chen, G., Chen, G., Chen, G., Chen, G., Chen, R., Chen, Z., Chowdhy, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhy, I., Christopoulos, C., Chen, G., Chen, R., Cavazos, S.R., Chacko, J., Chavez, D., Chen, B., Chen, R., Cavazos, S.R., Chacko, J., Chavez, D., Chen, A., L., Ding, Y., Dinh, H. H., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Garza, N., Gill, R., Gorrell, J.H., Geverar, N., Gunzartne, P., Hale, S., Hanilton, K., Haris, M., Haris, M., Hale, S., Hanilton, K., Haris, M., Haris, M., Hale, S., Hanilton, K., Haris, M., Hale, S., Hanilton, K., Haris, M., Haylak, P., Hawes, A., Hernandez, J., Harratae, P., Hale, S., Hanilton, K., Harisson, E., Kelly, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Joudah, S., L., Li, J., Li, Y., Johnson, R., Jolivet, S., Juudah, S., L.C., Lewis, L.C., Lewis, L.C., Lewis, L.C., Liu, J., Liu, W., Louse, M., Haris, M., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Wartin, R., Martinez, E., Marsen, M., Martinez, E., Marsen,
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Submitted (10-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                            Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROGRESS ***, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC130437 201416 bp DNA linear HTG 10-4
Homo_sapiens chromosome 3 clone RP11-740L19, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1.
                                                                                                                                                                                               (bases 1 to 201416)
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RESULT 9
AC022912
                                                                                                                                                                                                                                       Db 174985 AAGAAAAAATCTAGACAGGCA 174965
                                   KEYWORDS
                                                        VERSION
                                                                           ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
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ORGANISM
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                                                                                                                                                                                                                                                                             1 AAGAAAAATCTAGACAAGCA 21
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                  unordered pieces.
AC022912
AC022912.3 GI:7596818
                                                                                                             AC022912 218859 bp DNA linear HTG HOMO Sapiens clone RP11-740L19, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                          63751 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-primer Bodipy: Infinity% of reads Chemistry: Dye-terminator Big Dye: Infinity% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 20030 bases at least Q40
Consensus quality: 216627 bases at least Q30
Consensus quality: 233347 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: HDIU Center clone name: RP11-740L19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine Center code: BCM
              sapiens.
                                   HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                       Conservative
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9724
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2156
4276
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP11-740L19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                        88.2%;
95.2%;
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201416: contig of 53248
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gap of unknown length
contig of 49035 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length
contig of 16418 bp in
gap of unknown length
contig of 18703 bp in
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                                                                                                                                                                                                                                                                                                                     Mismatches
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NCE, 34
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Snoor

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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COMMENT
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-740L19
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 19, 2000 this sequence version replaced g1:7158108. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., McPheeters, R., McPheeters, P., Olivar, T. M., Peterson, K., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Piarne, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, Y., Raymond, C., Riley, R., Rothman, N., Rothman, R., Stojanovic, N., Subramanian, A., Talamas, J., Tefave, S., Theodore, J., Rothman, N., Subramanian, A., Talamas, J., Tefave, S., Theodore, J., Martin, M., Subramanian, A., Talamas, J., Tefave, S., Theodore, J., Martin, M., Subramanian, A., Talamas, J., Tefave, S., Theodore, J., Martin, M., Subramanian, A., Talamas, J., Tefave, S., Theodore, J., Martin, M., Martin, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 0.960731
Consensus quality: 186472 bases at least Q40
Consensus quality: 198582 bases at least Q30
Consensus quality: 206779 bases at least Q20
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Chemistry: Dye-terminator Big Dye; 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 185000; agarose-fp
Insert size: 215559; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: 740_L_19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
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1311 23
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7846:
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9092: gap
10112:
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3783:
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                                                                                      8992:
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                                contig of 1046 bp in length of 100 bp
                                                                                                                                                                                                     contig of 1096 of 100 bp
                                                                                                                                                                                                                                                                                                                of 100 bp
contig of 1186 bp in
                                                                                                                                                                                                                                                                                                                                                                                              of 100 bp
contig of 1322 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 100 bp
contig of 1051
                                                                                                                   contig of 1481
of 100 bp
        contig
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                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109033 109132:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170985 171084: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151791 151890: gap of 100 bp
151891 170984: contig of 19094 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84413 84512:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95986 96085:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20862 20961: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73768 73867:
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1311. .2361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-740L19"
/clone=lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                  2462.
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
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35211: contig of 1796 bp in length
35311: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15027: gap of 
16366: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13046: gap of 
14927: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11648: gap of 12946: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10212: gap of 100 bp
11548: contig of 1336 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29006:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25490:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22646:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18096:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16466:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50283:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40423:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56649:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109032:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193704:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311: gap of 100 bp 40323; contig of 5012 bp in length 423: gap of 100 bp 44661; contig of 4238 bp in length 761: gap of 100 bp 50183; contig of 5022 bp in length 502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218859:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9132: gap of 100 b
120785: contig of 11653
1885: gap of 100 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 bp
95985; contig of 11473 bp in
185; gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367: gap of 100 bp
84412: contig of 10545 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283: gap of 100 bp
56549: contig of 6266 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22546: contig of 1585 bp in length 46: gap of 100 bp 25390: contig of 2744 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60: gap of 100 bp
73767: contig of 10107 bp in length
67: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33315:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90: gap of 100 bp
28906: contig of 3416 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63560: contig of 6911 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20861:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17996:
                                                                                                  .8992
                                                                                                                                                                                                                                                                                                                                                                                                                  .3783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ontig of 12947 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p of 100 bp
contig of 1339 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p of 100 bp contig of 1881 k
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 2765 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 1530 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 22620 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ap of 100 bp contig of 19267 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 25055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp
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TITLE JOURNAL

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Db 146022 AAGAAAAATCTAGACAGGCA 146042
                                                                                                                                                                                                                                                                                                                                      1 AAGAAAAATCTAGACAAGCA 21
                                                                    Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi; Mammalla; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 274349)
Waterston,R.H.
                                                                                                                                                                                                              ACO93623 274349 bp DNA linear HTG 07-SEP-20
                                                      The sequence of Homo sapiens clone
                                                                                                                                                                        AC093623.1 GI:15487445
                                                                                                                                                                                                   PROGRESS ***, 49 unordered pieces.
                          (bases 1 to 274349)
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"assembly_fragment" 109133. .120785
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
96086. .109032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
84513. .95985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33416. .35211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note-"assembly_fragment"
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53661. .73767
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|6467. .17996
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently * consists of 49 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 248392 bases at least Q40 Consensus quality: 257485 bases at least Q30 Consensus quality: 262193 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-primer ET; 1% of reads
Chemistry: Dye-terminator Big Dye; 99% of
Assembly program: Phrap; version 0.990319
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Submitted (07-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center
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1489: gap of unknown length
2556: contig of 1067 bp in length
2656: gap of unknown length
3865: contig of 1209 bp in length
3965: gap of unknown length
5038: contig of 1073 bp in length
5138: gap of unknown length
6762: contig of 1624 bp in length
6762: contig of 1624 bp in length
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REFERENCE AUTHORS TITLE

REFERENCE

Waterston, R.H.

JOURNAL

Unpublished

VERSION KEYWORDS

HTG;

HTGS_PHASE1.

ACCESSION DEFINITION

AC093623

SOURCE

ORGANISM

Homo sapiens

Homo sapiens.

LOCUS AC093623/c

RESULT 10

Matches Query Match

Conservative

Best Local Similarity

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note-"assembly_fragment"

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                                                     /note="assembly_name:Contig28"
6863. .8029
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1490. .2556
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/db_xref="taxon:9606"
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/note="assembly_name:Contig31"
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8: gap of unknown length

3: contig of 8825 bp in length

3: contig of maknown length
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Best Local Similarity
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                                                                                                                                                                          Olyza Surre. 2016. A04. Clone:OJISO6. A04. Clone:OJISO6. A04. Clone:OJISO6. A04. Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Eiliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Fhrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                             APO05572 113940 bp DNA linear HTG 24-JUL-2002 Oryza sativa (japonica cultivar-group) chromosome 9 clone OJ1506_A04, *** SEQUENCING IN PROGRESS ***, in ordered pieces. APO05572
         published Only in Database (2002)
2 (bases 1 to 113940)
2 sasaki,T., Matsumoto,T., Hattori,M., Sakaki,Y. and Katayose,Y.
Direct Submission
Submitted (23-JUL-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                                  Sasaki,T., Matsumoto,T., Hattori,M., oryza sativa nipponbare(GA3) genomic clone:OJ1506_A04
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/note="assembly_name:Contig32"
10542. .11788
/note="assembly_name:Contig34"
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19157. .20355
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39387. .42070
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23849. .25791
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95.2%;
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Pred. No. 1.5e+02;
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Length 274349; Indels

0;

Gaps

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FEATURES

source

Sakaki,Y. and Katayose,Y. DNA, chromosome 9, BAC

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The nucleotide sequence of this BAC clone was generated by combining Monsanto and RCP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced by the finished sequence.

* This sequence will be replaced by the finished sequence.

* This sequence will be preserved.

* This sequence will be preserved.

* This sequence will be preserved.

* Location/Qualifiers

1 11340
                                                                                                                                     Barth,A.L.
Direct Submission
Submitted (07-DEC-1995) Molecular and Cellular Biology, University of California, Berkeley, Rm. 265 LSA, Berkeley, CA 94720, USA (bases 1 to 2052)

4 (bases 1 to 2052)
                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygil; Neopterygil; Teleostel; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 2052)

Barth, A.L., Justice, N.J. and Ngai, J.

Asynchronous onset of odorant receptor expression in the developir zebrafish olfactory system
Neuron 16 (1), 23-34 (1996)
                            of California, Berkeley, Rm. 265 LSA, Berkeley, CA 94720, Sequence updated by submitter On Oct 24, 2000 this sequence version replaced g1:1151128
                                                                                                                                                                                                                                                                                                         9292725
                                                                        Submitted (08-JUL-1997) Molecular and Cellular Biology, University of California, Berkeley, Rm. 265 LSA, Berkeley, CA 94720, USA
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                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                     Noncoordinate expression of odorant receptor genes tightly linked in the zebrafish genome Neuron 19 (2), 359-369 (1997) 97436752
                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 2052)
Barth,A.L., Dugas,J.C. and Ngai,J.
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Location/Qualifiers
1. .2052
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/db_xref="taxon:39947"
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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/translation="mlkivtraghtarisniaahllrtspslltrtttttttreppstssflunghlkkpkpgeelkitfilkdgsqktyevcegetildiaqghuldmegacggsc
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                                                                                                                                               /note="ORF YPL252c"
                                                                                                                                                           LNINWANLQKQNLERQVNHESQLRKDFIAFKEAKLKSMENLTNKHRELLDQIATLQSE
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                                                                                                                         /codon_start=]
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/note="ORF YPL253c"</pre>
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YFRAYPLPYCAENTIIOCYCDHISITSLACTNRAPYSIPAFVLAWVALLTPLAFIVFS
YCAIILAVVLRISSTQARKKTESTCSPGUIIIALYFLAFGFIYESSNIGIYFSYDLRLA
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/db_xref="taxon:4932"
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/protein_id="AAC60253.1"
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/db_xref="taxon:7955"
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Z73609 U00094
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EKGRNLVVVVVRVSRDGEVRKRCAAMFDILAVCPARVTIFSIGGGLSIDTRSAYFV"
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/note="ORF YPL251w"
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/note="ORF YPL253c"
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FEKHSISLDSKXLVIIEMCLEDLPLNFSCDEHPNLPHSGMGIIKVQFFPRDSKSDGNND
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                                                                                                       1138. .1148
/note="ARS-consensus"
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/db_xref="taxon:4932"
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                        Length 2411;
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae.
Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-NOV-1995) Thomas M. Pohl, GATC G
Fritz-Arnold-Str. 23, Konstanz, 78467, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pohl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharom Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; SRP68 protein; SUI3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fritz-Arnold-Str. 23, 2 (bases 1 to 37808)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 37808)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative protein"
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/db_xref="GI:1061235"
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/db_xref="taxon:4932"
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ATLQAELDQNLILKRQESQELYNNKLIFWENELQIMENVEPDHEITEEISQLKKTLQE
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/protein_id="cAA91591.1"
/db_xref="GI:1061236"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                               TPHGSLRESLIKFLAEKDTIYOKQYVITLQFVFLSDDEFSQDMLLDYSHNDKDSIKLK
FEKHSISLDSKLVIIENGLEDLPLNFSCDEHPNLPHSGMGIIKVQFFPRDSKSDGNND
                                                                                                                                                                                                                                                                               LNINWANLOKONLEROVNHESOLRKDFTAFKEAKLKSMENLTNKHRELLDQIATLOSE
SEKLHKEIMDIDROAEYSEONISEINENIKOLELANNPLISKSLONSODLEHLONOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2448. .4391)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNGNNETAEPQGPNQRIDLGAMIEELTSLLGKESWTKYAQIISLFILGKLSRKELSNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="SWISS-PROT:Q12060"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="cosmid library (A. Goffeau, Belgium)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="XVI"
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/db_xref="GI:1061237"
                                                                                                       complement(4748. .5266)
                                                                                                                          VNKLLTISEEVQTQLCKRKKKLT"
                                                                                                                                                                                                                                                          NLKEMASKQEKFYNDTYNTVEKELLRSRRLENSIIEQKGTMRCYAYVMEQNLPENLLF
                                                                             /codon_start=]
                                                                                                                                                       {\tt PVPVDFYFIELNNLKSIEQFDKSIFKKESCETPIALVLKKLISDTKSFFLLNLNDSKN}
                                                                                                                                                                                                                                  DYENGVITQGLSEHVYKFNRVIPHLKVSEDKFFTQEYSVYHDMCLNQKKNFNLISLST
                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q12045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=]
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/db_xref="SPTREMBL:Q12184"

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//db_xre-"Streem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOWQILFNCILAIGAWCIEGESTDIDVTYYQNAKSHLISKVEESGSIILVTALHLLSR
YTQWRQKTNTSYNFHSESIRMAISLGLNRDLPSSFSDSSILEQRRRIWWSVYSWEIQL
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QLSLIIYVLRDFFTNFTQKKSQLEQDQNDHQSYEVKRQSIMLSDAAQQTVMSVSSSYMD
HNVTPYFAWNCSYYLFNAVLVPIKTLLSNSKSNAENNETAQLLQQINTVLMLLKKLA
TFKIQTCEKYIQVLEEVCAPFLLSQCAIPLHISYNNSNGSAIKNIYGSATIAQYPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEENVNNISVKYVSPGSVGPSPVPLKSGASFSDLVKLLSNRPPSRNSPVTIPRSTPSH
RSVTPPLGQQQLQSLVPLTPSALFGGANFNQSGNIADSSLSFTFTNSSNGPNLITTQ
TNSQALSQPIASSNVHDNFMNNEITASKIDDGNNSKPLSPGWTDQTAYNAFGITTGMF
                                                                                                                                                                    /product="putative protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNVNRLPTMITDRYTLASRSTTSRLLQSYLNNFHPYCPIVHSPTLMMLYNNQIEIASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFYQDNV NKDAVTDRLASVETDMPLTLRQHRISATSSEESSNKGQRQLTVSIDSAAHHDNSTIP LDFMPRDALHGFDWSEEDDMSDGLPFLKTDPNNNGFFGDGSLLCILRSIGFRPENYTN
GPSPFGMSGNTTNGGNSKRNSGCDLSATYYASRSPMYSPLDFSPPVFSPNHSQLQQAR
                                                                                                                                                                                                                                                                                                                                                                                            complement(14010. .15581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTTTMDDVYNYLFDDEDTPPNPKKE"
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                                                                                                                       db_xref="SPTREMBL:Q12523"
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IDELLNINKEQVSTASLLERDSKAKGRKGWTGFKKVFK"
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COMPLIEMENT (8054. .10738)
                                                   translation="MDPFHNGNKRSSISFGSSQRQPYNKNNYLSGTNGPSSAAQDQGR
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CDS

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFGSLVLIMITVTRKMVSMILSIIVFGKSVRFQQWVGMFIVFGGITWEALNKKKANIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYVKTQLIAHDSEVFDVRFLTKSTQLFASCGGDGSVRVFDLRSLAHSTITYEPPSSSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYAANIPVVSNLMNPSMASVCEYQSHYPLFGLDWSADDYVCLGSYKEDSRNKLQVLHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGCVSGKKFQNVRVL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:Q12270"
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Search completed: March 17, 2003, 11:31:31 Job time : 548.495 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                               10:
11:
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22
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00000	Result
987654821	No.
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0444UUUU	
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2483 370 412 412 434 507 674	Query Match Length DB
2222222224	DB
ABQ69157 ABA112703 ABA118135 ABA118136 ABV37860 ABV37860 ABV38334 AAS30250 AAS30251 AAS26974	
Listeria monocytog Human nervous syst Human nervous syst Human prostate exp Human prostate exp Human prostate exp DNA encoding rena DNA encoding rena DNA encoding rena	Description

PT PT

New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides,

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544444333334 5443210988765443	3321	19 20 21 22 23	10 11 12 12 13 14 15 16
17.2 17.2 17.2 17.2 17.2 17.2 17.2 17.2			17.2 17.2 17.2 17.2 17.2 17.2
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11298 11298 11298 11298 11298 11298 11357 21742 21742 24512 24512 24512 24512 24512	4081 4081 4131 4258 5552 6716 7202 7202 9615	1588 1622 2713 2961 2963 3138	674 674 674 782 786 831 831 1372
18 19 21 21 22 14 21 21 21 21 22 22 22 22 22 22			
AAT86756 AAV94461 AAR20937 AAA34815 AAR92144 AAA71024 AAR20938 AAR34816 AAA34816 AAA34816 AAA757749 AAR71749 AAR71749	AAF77688 ABL16178 AAF77689 AAK67062 AAA58309 ABL33783 ABL33783 ABA19579 AAK71750 AAL36590	AAC35087 AAK83087 ABL24452 ABQ77508 ABL22334 ABL223782	AAS26975 AAS33485 AAS33486 AAS37775 ABQ73702 ABQ43712 ABQ43713 ABQ43713 ABQ43713
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Human high affinit Human beta subunit Human high affinit Human adenosine re Human IGERB gene S Human FCERI beta C Human high affinit Human nervous syst Human immune/haema Atopy related gene	wild- phila varia immur pyCSP immur immur immur	Arabidopsis thalia Arabidopsis thalia Human immune/haema Drosophila melanog Human cytokine rec Drosophila melanog Drosophila melanog	genoming ncoding ncoding ncoding ted sec colon nucleot prosts

ALIGNMENTS

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WPI; 2002-332479/37.	Kunst F, Glaser P;	 (CNRS) CNRS CENT NAT RECH SCT	(INSP) INST PASTEUR.	04-OCT-2000; 2000FR-0012697.		04-OCT-2001; 2001WO-FR03061.	11-APR-2002.		WO200228891-A2.		Listeria monocytogenes 4b.		infection; ds.	Antibacterial; Listeria: food contamination: mutational analysis:	the section of the se	Listeria monocytogenes 4b contig DNA seguence #1023		29-AUG-2002 (first entry)		ABQ69157;		ABQ69157 standard; DNA; 2483 BP.	JT 1

2000US-0222-2000US-0225447. 2000US-0225757.

2000US-0224519. 2000US-0225213.

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RESULT 2
ABA12703/c
ID ABA12703 standard; cDNA; 370
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   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                   04-FEB-2000
24-FEB-2000
02-MAR-2000
16-MAR-2000
17-MAR-2000
18-APR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
30-JUN-2000
07-JUL-2000
07-JUL-2000
07-JUL-2000
07-JUL-2000
07-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to nucleic acid sequences (ABO67188-ABO71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the printed specification, but was obtained in electronic fo directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                          Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2483 BP; 771 A; 651 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-Listeria vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies and modulators
                                                                                                                                                                                                                                                                                                                                                                                                         23-JAN-2002 (first entry)
                                                                                                                                                                                                                 17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                  Human nervous system related polynucleotide SEQ ID NO 1710.
                                                                                                                                                                                            31-JAN-2000;
                                                                                                                                                                                                                                     16-AUG-2001
                                                                                                                                                                                                                                                           WO200159063-A2
                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                   neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAGAAAAAATCTAGACAAGCA 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID 1970; 180pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
2000US-0190076.
2000US-020515.
2000US-020515.
2000US-0209467.
2000US-0214686.
2000US-0215135.
2000US-0216647.
2000US-0217487.
2000US-0217487.
2000US-0217496.
2000US-021963.
2000US-021963.
2000US-021963.
2000US-0220963.
2000US-0220963.
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2000US-0186350.
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2000US-0180628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.9%;
                                                                                                                                                                                                                                                                                                    infection; nephrotropic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.8; DB 24
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         699 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
     01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
    13-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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23-AUG-2000;
30-AUG-2000;
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25-SEP-
25-SEP-
26-SEP-
27-SEP-
27-SEP-
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14-AUG-2000;
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05-SEP-2000;
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22-AUG-2000;
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08-SEP-2000;
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06-SEP-2000;
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2000US-0225757 2000US-0225758 2000US-0225758 2000US-0225681 2000US-0226681 2000US-02226881 2000US-022934 2000US-022934 2000US-022934 2000US-022934 2000US-022934 2000US-023124 2000US-023124 2000US-023124 2000US-023124 2000US-0231413 2000US-0231413 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231968 2000US-023396 2000US-023396 2000US-023396 2000US-0233063 2000US-023401 2000US-023499 2000US-0236867 2000US-0236870 2000US-0236867 2000US-0236870 2000US-0241888 2000US-0241888 2000US-0241888 2000US-02446477 2000US-02446477 2000US-0246477

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CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant)agonists are useful CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC and parasitic infections.
       08-NOV-2000

08-NOV-2000

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17-NOV-2000

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17-NOV-2000
01-DEC-2000
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                                                                                                                                                          Claim 1; SEQ ID NO 1710; 1701pp +
                                                                                                                                                                              useful for preventing, cancers and metastases
                                                                                                                                                                                               Nucleic acids encoding
                                                                                                                                                                                                                    P-PSDB; ABB16377
                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                             2001-541565/60.
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2000US-0246610.
2000US-0246611.
2000US-0246613.
2000US-02469207.
2000US-0249208.
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2000US-0250391.
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2000US-0249245.
2000US-0249264.
2000US-0249265.
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2000US-0251479.
2000US-0251856.
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2000US-0249213
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                                                                                                                                                                                                                                                                    SCI INC
                                                                                                                                                                                       3224 human
diagnosing
                                                                                                                                                                                                                                                 Ruben
                                                                                                                                                                                                                                                 SM;
                                                                                                                                                           Sequence Listing; English
                                                                                                                                                                                       and/or treating nervous
                                                                                                                                                                                                 nervous system antigen polypeptides,
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RESULT 3
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 14 - AUG
14 - AUG
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                                                                                                                                                                                                                                  26-JUL-2000
26-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-2000
07-JUN-2000
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24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 370 BP; 130 A; 59 C; 60 G; 120 T; 1 other;
                                                                                                                                                                                                   14-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disease; infection; nephrotropic; gene therapy; vaccine;
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2000US-0225968
2000US-0224518
2000US-0224519
2000US-0224519
2000US-0225213
2000US-0225213
2000US-0225266
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2000US-0225758
2000US-0225759
2000US-0225759
2000US-0225759
2000US-0225759
2000US-0226681
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2000US-0198123.
2000US-0205515.
2000US-0209467.
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2000US-0217487
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2000US-0218290
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94.78;
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Pred. No. 3.
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Matches 18
                                                                                                                                                                                        The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infectious.
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17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding useful for preventing, cancers and metastases
                                                                                                                      Sequence 412 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 10466; 1701pp + Sequence Listing; English.
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220
               1 AAGAAAAAATCTAGACAAG 19
AAGAAAATATCTAGACAAG 202
                                                                        Similarity
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                                                                     79.1%;
94.7%;
                                                                                                                  A; 69 C;
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                                                          0;
                                                                        Score 17.4;
Pred. No. 3
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                                                                                                                    71 G; 135 T; 0 other;
                                                          Mismatches
                                                                        .8e+02
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                                                                                    Length 412;
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3-0241786. 3-0241787.

2000US-0237040. 2000US-0239935. 2000US-0239937.

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ABA18136/C
ABA18136;

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ABA18136;

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ABA18136;

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ABA18136;

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DT 23-JAN-2002 (first entry)

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Human nervous system related poly,

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Whith iteration in a misistic interprotective interprotec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurological disease; infection;
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    08-NOV-2000
17-NOV-2000
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20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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20-OCT-2000;
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                 2000US-0232398.
2000US-0232396.
2000US-0232401.
2000US-0233063.
2000US-0234297.
2000US-0234997.
2000US-0234998.
2000US-0234998.
2000US-0235836.
2000US-0235836.
2000US-0236336.
2000US-0236360.
2000US-0236360.
2000US-0236360.
2000US-0241786.
2000US-0241786.
2000US-0241786.
2000US-0246477.
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2000US-0246611.
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2000US-0246523.
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2000US-0231413.
2000US-0231414.
2000US-0232080.
2000US-0232081.
2000US-0232081.
2000US-0232397.
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ABV37860/C
ID ABV378
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AC ABV378
AC ABV378
DT 16-SEP
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DE Human
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KW Human;
KW Pharma
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                                                                                                                                                                                    RESULT 5
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08-DEC-2000;
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01-DEC-2000;
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11-DEC-
05-JAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases –
              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                              disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breas and ovarian cancer and other cancers of the adrenal gland, bone, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
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17
17
                                                                                                                                                                                                                                                                                                                                                       Sequence 412 BP;
                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format dir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel genes (ABA11004-ABA21534) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                             Human prostate expression marker cDNA 37851.
                                                                                             16-SEP-2002
                                                                                                                           ABV37860;
                                                                                                                                                       ABV37860 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 10467; 1701pp + Sequence Listing; English
                                                                                                                                                                                                                                   220
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                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                              1 AAGAAAAATCTAGACAAG 19
                                                                                                                                                                                                                                                                                                                                                                                     WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                   AAGAAAATATCTAGACAAG 202
                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                           Conservative
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2001US-0259678
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2000US-0251030.
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2000US-0249300
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2000US-0249297.
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2000US-0251479.
                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                          79.18;
94.78;
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                                                                                                                                                                                                                                                                                                            Score 17.4;
Pred. No. 3
                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                          135 T; 0 other;
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                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                            Length 412;
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                                                                                                                                                                                                                                                                                                                                                                                                      format directly
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                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crohn's
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Дb QУ

WO200160860-A2

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(g) determining whether prostate cancer has metastasized and patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 7745-7746; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-662795/76.
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18-JUL-2000;
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25-MAY-2000;
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                                                                                                                                                                                                           Human prostate expression marker cDNA 58325
                                                                                                                                                                                                                                                                                               ABV58334;
                                                                                                                                                                                                                                                                                                                                      ABV58334 standard; cDNA; 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 434 BP; 130 A; 78 C; 76 G; 150 T; 0 other;
                                                                                                                                                 pharmacogenomic
                                                                                                                                                                   Human; prostate
                                                                                                                                                                                                                                                        13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (g) determining whether prostate cames and more of prostate cancer in (h) assessing the aggressiveness or indolence of prostate cancer in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAGAAAAATCTAGACAAGCAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                      marker;
                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.2%;
86.4%;
                                                                                                                                                    gene;
                                                                                                                                                                     cytostatic; carcinogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monahan JE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.2; DB 23
Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23;
                                                                                                                                                                       pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 434;
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RESULT 7
AAS30250
ID AAS3
XX AAS3
XX AAS3
XX DT 21-N
DE DNA
XX Huma
KW Card
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Best Local 9
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                                                                                                      Human; antlinflammatory; neuroprotective; immunomodulator; vulnerary; cardiovascular; cytostatic; nephrotropic; antianaemic; nephritis; immunosuppressive; kidney disorder; renal failure; hypertension; cardiovascular disorder; myocardial infarction; blood disorder; anaemia; blood coagulation disorder; electrolyte imbalance disorder; cancer; hyponatraemia; hypertalaemia; neoplastic disorder; nephtoma; autoimmune disease; inflammatory disease; reproductive system disorder; endocrine disorder; neural activity; neurological disorder; wound healing; respiratory disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
           02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                               WO200155328-A2
                                                                                                                                                                                                                                                                                                 DNA encoding
                                                                                                                                                                                                                                                                                                                                   21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         AAS30250 standard; DNA; 674 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 507 BP; 179 A; 98 C; 93 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (e) selecting a composition for inhibiting prostate cancer in a patier (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-662795/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 AAGAAAAACACTAGTCAAGCAA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAGAAAAATCTAGACAAGCAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is also useful as a pharmacodyanamic or pharmacogenomic marker.
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31-JAN-2000;
04-EEB-2000;
24-EEB-2000;
02-MAR-2000;
16-MAR-2000;
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06-DEC-2000
06-DEC-2000
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                                                                                                                                           New polynucleotides and polypeptides, useful for diagnosing, treating, preventing or prognosing e.g. kidney, cardiovascular, blood, electrolyte imbalance or neoplastic disorders, autoimmune diseases, cancers -
The invention relates to novel nucleic acids and polypeptides useful diagnosing, treating, preventing and/or prognosing disorders related these polypeptides. The polynucleotides are especially useful in the diagnosis, prognosis, prevention and/or treatment of diseases which include kidney disorders (e.g. renal failure or nephritis),
                                                                                                            Claim
                                                                                                                                                                                                                                   WPI;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immunosuppressive; antiarthritic; ds; antirheumatic; cytostatic; cardiant; vascuropic; cerebroprotective; noutropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; cerebral ischaemia; angiogenesic corneal infection; wound healing; epithelial cell proliferative.
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2000US-0229345.
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The invention relates to isolated nucleic acid molecules and their ce encoded secreted proteins. The nucleic acids and proteins are used to comprevent, treat or ameliorate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They care also used in diagnosing a pathological condition or susceptibility con a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in condition assays e.g. radioimmunoassays or enzyme linked condition condition assays or enzyme linked condition assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, comperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, viruses and fungicand ocular disorders e.g. corneal infection, and many other conditionation and condition and condition also dead to aid wound healing and epithelial cell proliferation, to
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11-NOV-2000
01-DEC-2000
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                                                                                                                                                                                                                                                                                     Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, haemophilia -
                                                                                                                                                                                                                                                             Disclosure; SEQ ID No 310; 601pp; English.
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                                                                                                                                                               28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
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16-MAR-2000;
17-MAR-2000;
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19-MAY-2000;
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86.48;
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2000US-0249211.
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Barash SC, Ruben SM;

WPI; 2001-476222/51.

Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder,

Disclosure; SEQ ID No 311; 601pp; English.

Alzheimer's disease, infections caused by bacteria, viruses and fungiand ocular disorders e.g. corneal infection, and many other disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintrain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be use as a food additive or preservative to increase or decrease storage capabilities fait context light rectains to the context of the context of context of the context of context of the context of encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autolimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral isohaemia, angiogenesis, nervous system disorders e.g. capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence is a genomic DNA encoding a partial novel secreted proteins relates to isolated nucleic acid molecules and their novel secreted protein be used of

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RESULT 11
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                                             cc encoding human secreted proteins (II). (I) and (II) are used to prevent, cc treat or ameliorate a medical condition in e.g. humans, mice, rabbits, cc goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with C inappropriate expression of secreted proteins. (I) and complementary cc sequences may also be used as DNA probes in diagnostic assays (e.g. co fsimilar nucleic acid sequences in samples, and so which patients may cc be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to cc down regulate expression and activity of (II). The anti-(II) antibodies and antagonists may also be used to cc down regulate expression and activity of (II). The anti-(II) antibodies and antagonists may also be used to cc disorders include for example: immune/autoimmune diseases (e.g. HIV cc in samples (e.g. by enzyme linked immunozorbant assay (ELISA)). The control of the secreted control of the secretions and antipolical arthritis calanomas, neoplasms of the breast or liver, Sezary syndrome and cc parkinson's disease and Charcot-Marier arrest technocrafia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel isolated nucleic acid molecules (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID No 768; 753pp; English.
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                               cerebrovascular disorders (e.g. cardiac arrest,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-451931/48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids and polypeptides, useful for diagnosing, preventing reating medical conditions -
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86.4%;
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                               tachycardia,
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encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate expression of secreted proteins. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to
                                                                                                                                                                                                                                                                                                                                                         New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; Alzheimer's disease; Parkinson's disease; human; multiple sclerosis; cancer; hyperproliferative disorder; info
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                                                                                                                                                                                                                                                                      The invention relates to novel isolated nucleic acid molecules (I)
                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID No 769; 753pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         healing; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.6e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 13
AAD37775/C
ID AAD37
XX AAD37
XX AAD37
XX 27-AU
DT 27-AU
XX Infla
KW Infla
KW neuro
XX Hunti
KW neuro
XX Hunti
XX 11-OC
XX Mus m
XX 11-OC
XX 11-OC
XX INFL
PT Viney
XX WPI;
XX New p
T treat
XX Claim
XX Claim
XX The i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC may also be used as diagnostic agents for detecting the presence of (II)
CC in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The
CC disorders include for example: immune/autoimmune diseases (e.g. HIV
CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
CC Parkinson's disease and Charcot-Marie-Tooth disease), cardio-
CC erebrovascular disorders (e.g. cardiac arrest, tachycardia,
CC angina and thrombosis), infections caused by bacteria, viruses and
CC fungi and ocular disorders (e.g. corneal infections). (I) and (II),
CC agonists, antagonists and antibodies can also be used to promote wound
CC healing, maintain organs before transplantation, and support cell culture
CC of primary tissues. AAS33043-AAS33486 represent human secreted protein
CC coding sequences, PCR primers, and related sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC at. ffr wine, inventor that a printed in electronic format directly from WIPO
Cat. fire wine, inventor that a printed contents of the content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huntington's disease; immunosuppressive; sepsis; nephrotropic; nootropic; neuroprotective; anticonvulsant; gene therapy; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inflammatory bowel disease; IBD; autoimmune disorder; arthritis; allergy; haematopoletic cell; thrombolytic; blood coagulation disorder; nephritis; asthma; organ rejection; graft-versus-nost disease; inflammation; shock; nerve disease; Alzheimer's disease; Parkinson's disease; antibacterial;
                                                                                                                                Claim
                                                                                                                                                                                   cells
                                                                                                                                                                                                            New polynucleotide associated with inflammatory bowel disease for treating disorders of the immune system, nervous system, hematopo
                                                                                                                                                                                                                                                                                         WPI; 2002-426280/45.
                                                                                                                                                                                                                                                                                                                                                                                             (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2000; 2000US-239712P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001; 2001WO-US32176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200231116-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD37775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD37775 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 674 BP; 144 A; 184 C; 145 G; 201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGAAAAATCTAGACAAGCAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAAAAATTTAAACAAACAA 158
                                                                                                                                                                                   ţ
                                                                                                                                                                                                                                                                                                                                            Sims JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                   modulate inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for mouse IMX5_09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                            Dubose RF,
                                                                                                                                214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                            Baum PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.6e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                          Hasel KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 674;
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                                                                                                                                                                                                                                                                                                                                            Hilbush BS
                                                                                                                                                                                                              hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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The invention relates to an isolated polynucleotide associated with inflammatory bowel disease (IBD). The invention is useful for manufacturing a medicament for use in preventing, treating, modulating, or ameliorating a medical condition which is IBD. The polypeptide and

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ABQ73702/c ID ABQ73702 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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sequences have cytostatic activity, and can be used in gene therapy, antisense therapy and in vaccines. CSNA and CSP sequences can be used for diagnosing and monitoring the presence and metastases of colon cancer in a patient, by determining an amount of CSP or CSNA in a sample of a patient, and comparing it to the amount of CSP or CSNA in a sample and normal control, where a difference in the amount of the nucleic acid or the polypeptide in the sample compared to that of normal control is associated with presence of colon cancer. CSP and CSNA sequences can be used for producing engineered colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shock, sepsis, arthritis and nephritis. The invention is useful to differentiate, proliferate and attract cells, leading to the regeneration of fissues and to treat central and peripheral nerve diseases e.g. Alzheimer's disease, Parkinson's disease, and Huntington's disease. The invention is useful in gene therapy. The present sequence is an extended sequence for mouse IMX5_09 which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotide are useful for treating disorders of the immune system e.g. autoimmune disorders, deficiencies or disorders of haematopoletic cells, to modulate haemostatic, or thrombolytic activity, treat blood coagulation disorders, allergic reactions and conditions, such as asthma, treat and/or prevent organ rejection or graft-versus-host disease and modulate inflammation, including inflammation associated with infection,
                                                                                                                                                                                                                                                                               Colon specific polypeptides and polynucleotides useful for detecting, diagnosing, monitoring, treating, staging and predicting cancers in humans having cancer and non-cancerous colon disease
                                                                                                                                                                                                                                                                                                                                                                                                 Sun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; colon specific nucleic acid; colon specific polypeptide; CSP; CSNA; colon specific gene; CSG; colon cancer; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 782 BP; 212 A; 180 C; 138
                                                                                                                                                                                     ABQ73695 to ABQ73841 represent human colon specific nucleic acid (CSNA) sequences, and ABP51826 to ABP51928 represent human colon specific
                                                                                                                                                                                                                                              Claim 1; Page 153; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000; 2000US-244717P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-OCT-2001; 2001WO-US51341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200248370-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human colon specific nucleic acid (CSNA) SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 AAAAAAAATCTAAACAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGAAAAATCTAGACAAGCAA
                                                                                                                                                                                                                                                                                                                                                            2002-583520/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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                                                                                                                                                                                                                                                                                                                                                                                             Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                 Ghosh MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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CC This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method CC is used: (1) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory CC systems etc., particularly by detecting mutations or single nucleotide cypes and for investigating cell differentiation. The method allows the CC AB013410-AB054121 represent genomic DNA sequences used to illustrate the CC the disclosure of the invention.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                     Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                   Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-371829/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-2001; 2001WO-EP10074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200218632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide for detecting cytosine methylation SEQ ID NO 30303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ43712 standard; DNA; 831 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 786 BP; 256 A; 118 C; 140 G; 272 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \ensuremath{\mathsf{CSNA}} sequences are useful for producing transgenic animals and cells and also in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 86.4 es 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.2%; Score 17.2; DB 24; Length 786; 86.4%; Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berlin K, Guetig D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.7e+02;
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SQ Sequence 831 BP; 125 A; 99 C; 281 G; 326 T; 0 other;

Query Match 78.2%; Score 17.2; DB 24; Length 831;
Best Local Similarity 86.4%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0;
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Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps

Qy 1 AAGAAAAAATCTAGACAAGCAA 22

Db 771 AAAAAAAAATCTAAACAACCAA 750

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Search completed: March 17, 2003, 10:50:47 Job time: 128.253 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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    16154066 seqs, 8097743376 residues
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22
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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20.4 20.4 20.4 18.8 18.8	Score
	Query Match Length DB ID
342 360 224 424	ength [
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10 AW740409 12 BG360474 10 AW740410 10 BB016617 17 BH670801 17 AZ009207	SUMMARIES
AW740409 BRI10552 BG360474 BRI10646 AW740410 BRI10553 BB016617 BB016617 BH670801 BOMLK25TF AZ009207 RPCI-23-3	Description

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ALIGNMENTS

	FEATURES SOUTCE	Fax: 3	12111 Tel: 3	Biomec	COMMENT Contac	JOURNAL Unpubl	and at	TITLE Genes	, Lewi	AUTHORS Raghav	REFERENCE 1 (ba	; Plan	ONGANISM GIOND		S	VERSION AW740	ACCESSION AW740409	DEFINITION BRIDE		RESULT 1 AW740409
/organism="Biomphalaria glabrata" /strain="BS-90" /db_xref="taxon:6526"	Location/Qualifiers 1342	rax: 301-770-4756 Email: nkr@helix.nih.gov. snajlsrulp@aol com	12111 Parklawn Dr., Rockville, MD 20852, USA Tel: 301-881-3300 ext.128	Blomedical Research Institute	Contact: Raghavan N	Unpublished (2000)	and after exposure to miracidia	Genes expressed by the hemocytes of Riomphalaria glabrata hoforo	Is, F.A. and Knight, M	Raghavan, N., Miller, A., Gardner, M., Kerlavage, A. R., FitzCorsid n. C.	(bases 1 to 342)	בעיימבו איטרים; איטרוניטכם; Gastropoda; Pulmonata; Basommatophora ; Planorbidae; Biomphalaria.	anipidatata giaorata	bloodfluke planorb.		AW740409.1 GI:7651688	AW740409	BRII0552 Biomphalaria glabrata (BS-90)-unexposed Lambda Zap Library	409 342 bp mRNA linear EST 27-APR-2000	

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DEFINITION
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Query Match
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BRI10646 Biomphalaria glabrata (BS-90)-unexposed Lambda Zap Library
Biomphalaria glabrata cDNA clone RBGIJ88TR, mRNA sequence.
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12111 Parklawn Dr., Rockville, MD 20852, USA
Tel: 301-881-3300 ext.128
Fax: 301-770-4755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Raghavan N
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Lewis,F.A. and Knight,M.
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nkr@helix.nih.gov, snailsrule@aol.com.
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//lab_host="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Total RNA was isolated from the hemocytes of
unexposed Biomphalaria glabrata (BS-90) snails and first
strand cDNA synthesized using an oligo-dT primer-linker
(XhoI). Second strand synthesis was followed by the
ligation of EcoRI adaptors. Following digestion with XhoI,
the completed, directional cDNA was cloned into Uni-ZAP
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/clone_lib="Biomphalaria glabrata (BS-90)-unexposed Lambda
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/clone="RBGIJ88TR"
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/strain="BS-90"
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95.5%;
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Pred. No. 1.1e+03;
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SOURCE VERSION

KEYWORDS ACCESSION

REFERENCE

COMMENT

JOURNAL TITLE AUTHORS

FEATURES

ORGANISM

RESULT 2 BG360474

BASE COUNT

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RESULT 3
AW740410
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                                                                                                                                          RESULT 4
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Biomphalaria glabrata cDNA clone RBGIH56TR, mRNA sequence.
AW740410
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                                                                             BB016617 RIKEN full-length enriched, adult male testis musculus cDNA clone 4930563D02 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: nkr@helix.nih.gov, snailsrule@aol.com
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0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                  Score 20.4; DB 10 Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, N. Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M. Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carning, P. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               turther details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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               99 a
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GAGAGAGAGATTCTCGAGTTĀATTAAAŤTAATCCCCCCCCCCCCC 3']. CDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

28 c 39 g 58 t
                                                                                                                                                                                       /note-"Site1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                         cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4930563D02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="testis"
/dev_stage="adult"
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Query Match

Score 18.8;

DB 10;

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Length 224;
      JOURNAL
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                            RPCI-23-365C18.TV RPCI-23 Mus musculus genomic clone RPCI-23-365C18
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 449)
                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                            AZ009207.1 GI:7084591
                                                                                                                                                                                        nouse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: sheared ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
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                                                                                                                                                                                                                                                                    DNA sequence.
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 86 c 66 g 107 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMLK25"
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Pred. No. 3.8e+03;
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                                                                                                                                                                                                                                                                                                            449 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
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Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB768795 RIKEN full-length enriched, B16 F10Y cells Mus musculus clone G370089D24 3', mRNA sequence.
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                                                                                                                                                                                                                                                        1 (bases 1 to 476)
1 (bases 1 to
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                  Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).

a 79 c 80 g 193 t
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/db_xref="taxon:10090"
/clone="RPCI-23-365C18"
/clone_lib="RPCI-23"
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Pred. No. 3.8e+03;
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BASE COUNT
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                                                                                                                                             AUTHORS
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11) 1757-1771 (2000)
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                                                                                                                                                                                                                        Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST433300 KV1 Medicago truncatula cDNA clone pKV1-18B14, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
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Unpublished (1999)
                            \mathtt{ESTS} from roots of Medicago truncatula 24 hours after inoculation with Sinorhizobium meliloti ^{\prime}
                                                                                                                                       VandenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L.,
                                                                                                                                                                                                                                                                                                                                        barrel medic
                                                                                                                                                                                                                                                                                                                                                                                            BF004802.1 GI:10705077
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                                                                                   Fraser, C.M.
                                                                                                          Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
                                                                                                                                                                                                    Medicago
                                                                                                                                                                          (bases 1 to 505)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex=mixed), (tissue_type=hippocampus, dev_stage=adult, sex=male), (tissue_type=whole body, dev_stage=9 days embryo, sex=mixed), (tissue_type=tung, dev_stage=13 days embryo, sex=mixed)  

embryo, sex=mixed)  

105 c 111 q 122 +
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                    Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Texas A&M University name: T268612e TIGR sequence name: MTIBJ07TK More information is available at: http://chrysie.tamu.edu/medicago Seq primer: SKmod (CTA gAA CTA gtt gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Plant Biology
University of Minnesota
20 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 612 624 2755
Fax: 612 625 1738
                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 Er from Amersham High quality sequence stop: 475.
                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)
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                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA447445.1 GI:2161115
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//note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhOI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."

a 93 c 103 g 164 t 1 others
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/dev_stage="24 hours post-inoculation with Sinorhizobium
meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV1-18B14"
/organism-"Homo sapiens"
/db_xref-"GDB:5982200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="KV1"
                                                                         Location/Qualifiers
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90.9%;
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AQ414714
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 7
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ414714 544 bp
RPCI-11-171019.TJ RPCI-11 Homo
                                                                                                                                                                                                                                                                                                                 library availability, please contact Pieter de Jong (pieter dedjong med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1\pmod{5}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                       Class: BAC ends.
                                                                                                                                                                                                                                                                           nttp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                     Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: hbe@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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113 c 91 g 169 t
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RPCII1 Human Male BAC Library"
97 c 100 g 158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:784582"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                           /db_xref="taxon:9606"
/clone="RPCI-11-171019"
                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="GDB:7565634"
                                                           /cell_type="Lymphocytes"
                                                                                    /sex="Male"
                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                       /clone_lib="RPCI-11"
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Pred. No. 3.7e+03;
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                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat.230.htm). For BAC library
availability, please contact Pieter de Jong (pdeJong@mail.cho.or
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 39 row: A column: 11
 AQ534621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Rat BAC End Sequences from Library CHORI-230 ECORI segment Unpublished (1999)
Other_GSSs: CH230-39A11.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CH230-39A11.TV CHORI-230 Segment 1 Rattus CH230-39A11, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., (
,A., Gebregeorgis,E., Overton,L., Russell,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Norway rat.
Rattus norvegicus
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                                                                                                                                                                                                                         /cell_type="Brain"
/note="Vector: pTaRBAC2.1; Sit
CHORI-230 Rat (BN/SSNHSd/MCW)
Pieter de Jong"
106 c 125 g 200 t
                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                                                                          /clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10116"
/clone="CH230-39A11"
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Pred. No. 3.7e
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Pred. No. 3.7e+03;
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DNA
                                                                                                                                                                                                                                                         Site_1: EcoRI;
CW) BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 de Jong (pdejong@mail.cho.org).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MD 20850, USA
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                                                                                                                                                                            549;
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                                                                                                                                                                                                                                                                        Site_2: EcoRI;
GSS 18-MAY-1999
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                          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1M0348C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0348C14 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
plasmid inserts
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from (pieter@dejong.med.buffalo.edu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other_GSSs: RPCI-11-353P23.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 567)
Zhao, S., Adams, M.D., Nierman, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPCI-11-353P23.TV RPCI-11
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AQ534621.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                 (bases 1 to 568)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medical Center Dr., Rockville, 301 838 0200 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Site_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="RPCI-11-353P23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-11"
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/db_xref="GDB:7635550"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                      Murinae; Mus
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COMMENT
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AQ534617
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Other_GSSs: RPCI-11-353P21.TJ
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 597)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                                                                                                                                                                                 RPCI-11-353P21.TV RPCI-11 Homo sapiens genomic clone RPCI-11-353P21
                              Unpublished (1997)
                                                            Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                       Map Building
                                                                                                                                                                                                                          Homo sapiens
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University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 568.
Location/Qualifiers
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Plate: 0348 row: C column: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                       DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib-"Mouse 10kb plasmid UUGClM library"
/sex-"Male"
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90.9%;
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FEATURES
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AUTHORS
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BH552202/c
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                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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Best Local Similarity
                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                Email: odtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                       Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOHON17TR
                                                                                                                                                                          Class: sheared ends.
                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523
                                                                                                                                                                                                                                                                                                                                            Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 710) Town, \text{C.D.} , Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOHQN17TF BOHQ Brassica oleracea genomic clone BOHQN17, DNA
                                                                                                                                                                                                                                                              Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH552202.1 GI:17803982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
BH552202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH552202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica oleracea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                              /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="reaxon:3712"
/clone="BOHQN17"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                          /clone_lib-"BOHQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ceil_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
a 107 c 115 g 174 t
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="RPCI-11-353P21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:7635548"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11"
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90.9%;
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Pred. No. 3.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                710 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
```

genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT 209 a 146 c 149 g 206 t

ORIGIN

Query Match

Best Local Similarity 90.9%; Pred. No. 3.5e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGAAAAATCTAGACAAGCAA 22

Qy 1 AAGAAAAATCTAGACAAGCAA 133

Db 154 AAGATAAAATCTAGATAAGCAA 133

Search completed: March 17, 2003, 13:09:20

Job time: 782.688 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 09:43:42; Search time 230.108 Seconds (without alignments) 3161.870 Million cell updates/sec

Title: Perfect score: Sequence: US-09-836-439-5 25

gctttctttgctgagagctcttcca 25

Scoring table:

IDENTITY_NUC Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_hb:*

4: gb_ba:*

4: gb_om:*

4: gb_ph:

9: gb_pr:

10: gb_rr:

11: gb_y:

12: gb_s:

13: gb_u

14: gb_s:

15: em_}

16: em_}

17: em_}

18: em_

21: em_

21: em_

23: em_

24: em_

25: em_

36: 33: em_

37: 37: 37: 37: 39: 44: gb_om:*
gb_pat:*
gb_pat:*
gb_ph:*
gb_pr:*
gb_pr:*
gb_pr:*
gb_yr:*
gb_yr:*
gb_un:*
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em_ba:*
em_bu:*
em_fun:*
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em_on:*
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Pred. No. is the number of results predicted by chance to have

em_htgo_other:* em_htgo_hum: *
em_htgo_mus: * em_htg_hum:*
em_htg_fin:*
em_htg_other:*
em_htg_mus:*
em_htg_pin:*
em_htg_pan:*
em_htg_nam:*
em_htg_ram:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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753	998	9920	2328 Astyar	UZIZ4Z Melopsi	084947 Xenotil	D84944 TILapia	941 Spathodu	084940 Sar	084938 0	84931 Dimidi	37213 Ostracio	1979	21974 Bufo pus	49158 Philautu	49157	249156 Polypeda	F249154 Indiran	F249152 Micrixal	F249151 Rana tem	F249150 Rana tem	249149 Rana cur	249148 Limnonec	249147 Limnonec	F249146	F249144 Nannophr	F249143 Euphlyct	249142 Sphaerot	249141	249140 Federvar	F249139 Feierva	249138 Laliosto	249137 Bookis	1249134 Mai	F249133 Mantella	F249129 Bufo	249131 Microhy	095437 Rattus	293018 Tetra	249155 Indirana	5171 Mouse ops	C013125 Mus musc	C031766 Mus mus	136698 Mouse op	Description	

ALIGNMENTS

REFERENCE AUTHORS TITLE		ORGANISM	SOURCE	SEGMENT	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	MUSOPS4	RESULT 1
<pre>1 (bases 1 to 269) Baehr,W., Falk,J.D., Bugra,K., Triantafyllos,J.T. and McGinnis,J.F. Isolation and analysis of the mouse opsin gene</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Mus musculus	Mus musculus (strain C56BL/6J) eye DNA.	4 Of 5	opsin.	M36698.1 GI:200149	M36698 X69175	Mouse opsin gene, exon 4.	MUSOPS4 269 bp DNA linear ROD 08-MAY-1993		

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RESULT 2
BC031766
                                                                                                   FEATURES
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTTCTTTGCTAAGAGCTCTTCCA 216
                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 31 Row: n Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC031766 2610 bp mRNA linear ROD 07-AUG-2
BC031766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 a 87 c 58 g
About 117 bp after segment 3.
                                                                                                                                                                                                                                                        Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEBS Lett.
89005694
                                                                                                                      analysis,
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                                                                                                                                                                                                                                                                                                                                                                            Sequencing Center
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order(M36697.1:170.
/gene="opsin"
                  /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="MGC:25387 IMAGE:4527040"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number=3
15. .254
/tissue_type="Eye, retina, mouse strain C57Bl\6"
                                                                                                 Location/Qualifiers
                                                                                                                      GenomeScan gene prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number=4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C56BL/6J"
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                            Series: IRAK Plate: 28 Row: e Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus, Similar to rhodopsin (retinitis pigmentosa 4, autosomal IMAGE:4500760, mRNA, complete cds. BC013125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
  identity to protein.
Location/Qualifiers
1. .3249
                                                                                                                               through the I.M.A.G.
                                                                                                                                                        Clone distribution: MGC clone distribution
                                                                                                                                                                                                                     Gunaratne, P.H., Garcia, A.M., Lu, X., Yoon, V.S., Kowis, C.R., Lawrence, S.,
                                                                                                                                                                                                                                                                                                          Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                              Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC013125.1
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                                                                                                                                                                                                                                                                  Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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/protein_id="AAH31766.1"
/db_xref="GI:21594395"
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IFFCYGQLVFTVKEAAAQQQESATTQKAEKEVTRMVIIMVIFFLICWLPYASVAFYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFRFGENHAIMGVVFT
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/translation="MNGTEGPNEYVPFSNVTGVVRSPFEQPQYYLAEPWQFSMLAAYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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/lab_host="DH10B"
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96.0%;
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Pred. No. 1
                                                                                                                                  Consortium/LLNL at: http://image.llnl.gov
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autosomal dominant), clone MGC:21585
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Martin, R.G.,
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                                                                                                                                                                                                                                                                                                                                                       Genome
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/db_xref="taxon:10090"

/organism="Mus musculus"

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SOURCE
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 9483)
al-Ubaidi.M.R., Pittler,S.J., Champagne,M.S., Triantafyllos,J.T., McGinnis,J.F. and Baehr.W.
McGinnis,J.F. and Baehr.W.
Mouse opsin. Gene structure and molecular basis of multiple transcripts
transcripts
J. Biol. Chem. 265 (33), 20563-20569 (1990)
                                                                                                                                                                                                                                                                                                                         91056108
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/tlssue_type="Eye, retina, mouse strain C57Bl\6"
/clone_lib="NIH_MGC_94"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                            Location/Qualifiers
            /gene-"MOPS"
                                   join(1434. .1794,3283. .3451,4525. .4690,4808. .5047,
                                                               /gene-"MOPS"
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                                                                                                                                            gene-"MOPS"
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                                                                                                                                                                                 'tissue_lib-"EMBL3"
                                                                                                                                                                                                  /t1ssue_type="liver"
/dev_stage="adult"
                                                                                                                                                                                                                                         /map-"chromosome 6"
                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                 organism-"Mus musculus"
/codon_start=1
                                                                                          'product-"opsin"
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Pred. No. 1.
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/product-"opsin"

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                                                                                         Indirana sp. 2 rhodopsin gene, exon AF249155
           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoldea; Ranidae;
                                                                            AF249155.1 GI:12247239
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/gene="MOPS"
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/db_xref="GI:200145"
/translation="mmotegphfyvpfsnvtgygrspfeqpqyylaepmqfsmlaaym
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fyfgptgcnlegffathwslavlavlairryvvckpmsnffgenhaimgyvft
wimalacaapplygmsryipegmqcscgidyytlkpevnnesfyiymfvyhftipmiv
iffcygglyftvkeaaaqqqesattokaekeytrmyimvifflichlpyasvafyif
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/gene="MOPS"
9092. .9097
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9303. .9309
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8205..8210
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7022. .7027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="MOPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="MOPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="MOPS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene≖"MOPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene≖"MOPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                number=3
                                                                                                                                                                                                                                                       93.6%;
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                                                                                                                                                                                                                                                                                                              2444 g
                                                                                                                                                                                                                                                         Score 23.4; D
Pred. No. 1.5;
                                                                                                                                                                                                                                           Mismatches
                                                                                                                      175 bp
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                                                                                                                       DNA
                                                                                                         ONA linear VF
4 and partial cds.
                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                      Length 9483;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                           FRANCE
                                                                                                                                                                                                                        Genoscope, 2 rue Gaston
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHOD gene; rhodopsin.
Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon nigroviridis rhod gene for rhodopsin. AJ293018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Molecular Biology and Medicine, rue Jeener and Brachet Gosselies B-6041, Belgium
                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                           Fischer,C.
                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                         Tetraodon nigroviridis gene for rhodopsin
                                                                                                                                                                                                                                                                                                                                                Fischer,C.
                                                                                                                                                                                                                                                                                                                                                                            Tetraodontidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ293018.1 GI:9909983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNI293018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 175)
Bossuyt, F. and Milinkovitch, M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 175)
Bossuyt, F. and Milinkovitch, M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs Reveal Co-variation between Larval and Adult Traits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                           (bases 1 to 1062)
                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 1062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
/codon_start=1
/product="rhodopsin"
/protein_id="CAC04526.1"
/db_xref="GI:9909984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number=4
3 54 c
                                                                     /gene="rhod"
                                                                                                    /gene="rhod"
                                                                                                                                      /organism="Tetraodon nigroviridis
/db_xref="taxon:99883"
                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                  (22-AUG-2000) Fischer C., Centre National de Sequencage, 2 rue Gaston Cremieux, CP5706, F-91057 Evry Cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPAFFAKSSSIYNP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=2
/product="rhodopsin"
/protein_id="AAC49798_1"
/db_xref="GI:12247240"
/translation="AEKEVTRMVVIMVVFFLICWVPYAYVAFYIFTHQGSEFGPIFMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Indirana sp./db_xref="taxon:147866"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="rhodopsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                      .1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.2%;
92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .>175
                                                                                                                                                                                                                                                                                                                                                                           Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21.8;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1062 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                      Bouck, J., Beunch, C., Blindge, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, Z., Chowdhry, I., Dathorne, S.R., David, R., Ding, Y., Dinh, H.H., Douthiwaite, K.J., Edwards, C.C., Elhaj, C., Escotto, M., Delaney, K., Bart, M., Ganer, T., Garza, N., Gill, R., Earnhart, C., Hodgson, A., Hogues, M., Holloway, C., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Garrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Marhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Massey, E., Marhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Martin, S., Martin, R., Nagyen, N., Notkerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oriekens, R., Parimus, E., Put, L., Ouiles, M., Ren, Y., Petez, L., Sonatke, T., Sonatke, A., Stanley, H., Stone H., Ston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                          Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Tamerisa, K.,
Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williams, G., Williams, R., Wooden, S.,
Williams, G., Williams, G., Williams, G., Williams, Williams, G., Williams,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC095437
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Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 128571 bases at least 040
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Consensus quality: 137554 bases at least 020
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Microhyloidea;
Microhylidae; Microhylinae; Microhyla.
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Bossuyt,F. and Milinkovitch,M.C.
Direct Submission
Bufo melanostictus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute Molecular Biology and Medicine, rue Jeener and Brachet 12, Gosselies B-6041, Belgium
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Bossuyt, F. and Millnkovitch, M.C.
Convergent Adaptive Radiations in Madagascan and Asian
Reveal Co-variation between Larval and Adult Traits
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/protein_id="AA649774.1"
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/translation="AEKEVTRMVVIMVIFFLICWVPYAYVAFYIFTHQGSEFGPIFMT
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/db_xref="taxon:147864"
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1 GCTTTCTTTGCTGAGAGCTCTTCCA 25
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Mantella madagascariensis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 175)
Bossuyt,F. and Milinkovitch,M.C.
Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mantella madagascariensis rhodopsin AF249133
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Bossuyt, F. and Milinkovitch, M.C
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                                                                                                                                                                                  Molecular Biology and Medicine,
Gosselies B-6041, Belgium
Location/Qualifiers
                                                                                                                                                                                                                           Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Molecular Biology and Medicine, rue Jeener and Brachet
                                                                                                                                                                                                                                                               Bossuyt, F. and Milinkovitch, M.C Direct Submission
                                                                                                                                                                                                                                                                                                                 Unpublished
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/db_xref="taxon:30335"
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/protein_id="AAG49776.1"
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                                                                                                                          /organism="Mantella madagascariensis"
/db_xref="taxon:111290"
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Pred. No. 52;
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Traits
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Rhacophoridae;
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TITLE
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                                                AF249136 175 bp DNA li
Boophis xerophilus rhodopsin gene, exon 4 and
AF249136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission

Direct Submission

Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute Molecular Biology and Medicine, rue Jeener and Brachet 12, Gosselies B-6041, Belgium
Location/Qualifiers
                              AF249136.1 GI:12247201
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1 (bases 1 to 175)

1 (bases 1 to 175)

Bossuyt.F. and Milinkovitch,M.C.

Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits
                                                                                                                                                                                                                                        Similarity
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Bossuyt,F. and Milinkovitch,M.C.
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
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VPAFFAKSSAIYNP"
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Pred. No. 52;
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AUTHORS
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                                                                                              2 (bases 1 to 175)
Bossuyt,F. and Milinkovitch,M.C.
Direct Submission
Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute of Molecular Biology and Medicine, rue Jeener and Brachet 12,
Gosselies B-6041, Belgium
                                                                                                                                                                                                              1 (bases 1 to 175)
Bossuyt, F. and Milinkovitch, M.C.
Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits
                                                                                                                                                                                                                                                                                                             Boophis tephraeomystax.
Boophis tephraeomystax
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                      Boophis tephraeomystax rhodopsin gene, exon 4 and partial cds
                                                                                                                                                                                                         Unpublished
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Boophis xerophilus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Matrachia; Anura; Neobatrachia; Ranoidea;
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Bossuyt,F. and Milinkovitch,M.C.
Direct Submission
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Bossuyt, F. and Milinkovitch, M.C.
Convergent Adaptive Radiations in Madagascan and Asian
Reveal Co-variation between Larval and Adult Traits
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Similarity 88.0%;
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/product="rhodopsin"
<1. .>175
                                           /organism="Boophis tephraeomystax"
/db_xref="taxon:68440"
                                                                                            Location/Qualifiers
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Rhacophoridae;
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BASE COUNT
ORIGIN
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AF249139
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Gosselies B-6041, Belgium
Location/Qualifiers
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Bossuyt, F. and Milinkovitch, M.C.
Direct Submission
Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laliostoma labrosum rhodopsin gene, exon 4 and partial cds {\tt AF249138}
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Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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Job time : 256.108 secs
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Bossuyt,F. and Milinkovitch,M.C.

Direct Submission

Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute of Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute (27-MAR-2000) Unit of Evolutionary Genetics, Institute (27-MAR-2000) Unit of Evolutionary Genetics, Institute (27-MAR-2000) Un
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Gosselies B-6041, Belgium
Location/Qualifiers
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Reveal Co-variation between Larval and Adult Traits
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Pred. No. 52;
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Ranidae;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ABL26659	23	702	71.2	17.8	ر. د	
	AAS36854	22	6912	72.8	18.2	4	
	AAC85295	22	3254	72.8	18.2	w	
	AAS77337	23	906	72.8	18.2	N	o
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ALIGNMENTS

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RESULT 2
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AAS77337;
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AAS77337;
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13-FEB-2002 (first entry)
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DNA encoding novel human diagnosti
XX
DNA HUMAN; chromosome mapping; gene ma
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11-OCT-2001;
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30-MAR-2001; 2001WO-US08631.
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31-MAR-2000; 2000US-0540217.
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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
                                                  Claim 1; SEQ ID No 13141; 103pp; English.
                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #13141.
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relates to isolated polynucleotide (I) and

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RESULT 3
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Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CR at fro.wipo.int/pub/piblished oct segmences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPANK; SAM; sterile alpha motif; PARP; insulin resistance; poly adenosine diphosphate-ribose polymerase; catalytic domain; ANK; ankyrin repeat; cytosol; insulin-responsive aminopeptidase; IRAP; GLUT4; adipocyte; insulin signalling pathway; hyperlipidaemia; glucose intolerance; atheromatous disease; atherosclerosis; obesity; cardiac insufficiency; coronary insufficiency; stroke; high blood pressure; non-insulin dependent diabetes; hypertension; high blood pressure; non-insulin dependent diabetes; hypertension;
                                                                                                   WO200077225-A1
                                                           21-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 906 BP; 243 A; 218 C; 269 G; 176 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hyperuricemia; Syndrome X; muscular dystrophy; muscle atrophy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse SPANK cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
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are absent, which alters the reading frame"
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insertion, which alters the reading frame"
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87.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New insulin signalling protein SPANK, useful for reducing body mass, glucose intolerance or insulin resistance and for preventing or treating obesity-related and muscle-related diseases
                                                                                                                                                                                                                                                                                                                                      2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPANK is useful for reducing body mass, reducing glucose intolerance or insulin resistance, for preventing or treating obssity-related diseases or disorders, such as obesity, cardiac insufficiency, coronary insufficiency, stroke, hypertension, atheromatous disease, atherosclerosis, high blood pressure, non-insulin dependent diabetes, hyperlipidaemia, hyperuricemia and Syndrome X and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEHO
                                                                                                          chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         also useful for preventing or treating muscle-related diseases or disorders, such as muscular dystrophy, muscle atrophy and muscle fatigue. Antibodies immunospecific for SPANK are useful for detec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPANK binds insulin-responsive aminopeptidase (IRAP) and modulates translocation of GLUT4 in the perinuclear region of adipocytes. It is an effector in the insulin signalling pathway in eukaryotic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 5A; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUN-1999;
                                                            fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3254 BP; 871 A; 746 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein comprises 3 domains:

(a) a SAM (sterile alpha motif) domain;

(b) a PARP (poly adenosine diphosphate-ribose polymerase) catalytic domain; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAB47023
                                                                                                                                                                                                                          17-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                            AAS36854 standard; DNA; 6912 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (c) an ANK domain composed of ankyrin repeats.
SPANK is a cytosolic protein which can poly(ADP-ribosyl)ate itself.
  WO200155321-A2
                         Homo sapiens
                                                   anti-infertility.
                                                                                                cerebrovascular disorder; nervous system disorder; bacterial infection;
                                                                                                                                                                          Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
                                                                                                                                                                                                  Human cardiovascular system antigen genomic DNA SEQ ID No 2354.
                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                             presence of SPANK polypeptide in a biological sample.
                                                                                                                                                                                                                                                                                                                                     TTATTTTGCTGAGAACTCTTCCA 2952
                                                                                                                                                                                                                                                                                                                                                              TTTCTTTGCTGAGAGCTCTTCCA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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87.0%;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        863 G;
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     14-SEP-2000;
11-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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30-AUG-
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22-AUG-2000;
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26-JUL-2000;
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17-MAR-2000;
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2000US-022547
2000US-0225757
2000US-0225757
2000US-0225759
2000US-022579
2000US-0226279
2000US-02268681
2000US-0227182
2000US-0227182
2000US-0227182
2000US-0229343
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2000US-0216880.
2000US-0217487.
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2000US-0180628.
2000US-0184664.
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2000US-0233065.
2000US-0234223.
2000US-0234274.
2000US-0234997.
2000US-0234998.
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2000US-0232080.
2000US-0232081.
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2000US-0230437.
2000US-0230438.
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2000US-0232401.
2000US-0233063.
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2000US-0218290.
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2000US-0231413
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2000US-0231243
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2000US-0225267
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2000US-0225213
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2000US-0232397,
                             2000US-0235834
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WPI; 2001-451930/48

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17.NOV-2000
11-NOV-2000
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20-OCT 2000
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
               Rosen CA,
                                                 (HUMA-) HUMAN GENOME SCI INC
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               Barash SC,
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2000US-0246476.
2000US-0246477.
2000US-0246478.
2000US-0246523.
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2000US-0241809.
2000US-0241826.
2000US-0244617.
2000US-0246474.
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2000US-0241221.
2000US-0241785.
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RESULT 5
ABL26659
YEAR A CONTRACT OF A CONTRACT 
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C detecting the presence or absence of a mutation in a cardiovascular

C system antigen polynucleotide. The treatable disorders include autoimmune

C diseases such as rheumatoid arthritis, hyperproliferative disorders such

C as neoplasms of the breast or liver, cardiovascular disorders such as

C cardiac arrest, cerebrovascular disorders such as cerebral ischaemia,

nervous system disorders such as Alzhehmer's disease, infections caused

by bacteria, viruses and fungi, ocular disorders such as corneal

C infection, endocrine disorders such as premature labour and infertility,

C gastrointestinal disorders such as premature labour and infertility,

C gastrointestinal disorders such as premature labour and of the polypeptides can also be used to aid wound healing, to

C pleuristy. The polypeptides can also be used to aid wound healing, to

C prevent skin aging due to sunburn, to maintain organs before

C transplantation, to regenerate tissues and in chemotaxis.

Note: The sequence data for this patent did not form part of the printed

Specification, but was obtained in electronic format directly from WIPO

at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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                                                                                                                                                                                                                                                                                         23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genomic polynucleotide SEQ ID NO 31450.
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                                                                                      WPI; 2001-656860/75.
                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 TTTCTTTGCTGATAGCGGTTCCA 669
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                                                                                                                                                         JС,
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2000US-0614150
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Pred. No. 1.9e+02;
"'Amatches 3;
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell

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RESULT 6
AAH51547/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; biallelic marker; single nucleotide polymorphism; SNP; MGSTII; microsomal glutathione S-transferase II; malate decarboxylase enzyme; DME1; ME1; cytochrome P450; glutathione reductase; GSHR; GSHS; GGT5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
Sequences AAH51110-AAH51593 represent human DNA fragments which contain biallelic markers. The sequences are related to various human genes including microsomal glutathione S-transferase II (MGSTII), malate decarboxylase enzyme (DMEI/MEI), cytochrome P450, glutathione reductase/synthase (GSHR/GSHS), flavin-containing monooxygenases (FMO),
                                                                                                                                    Polynucleotides comprising sequences from malate decarboxylase enzyme-related biallelic markers used for genotyping -
                                                                                                                                                                                          WPI; 2000-638353/61.
                                                                                                                                                                                                                           Blumenfeld M,
                                                                                                                                                                                                                                                                                             25-MAR-1999;
30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MGSTII related DNA containing a biallelic polymorphism SEQ ID 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475 TCTTTCCTGAGCGCTCTTCCA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TCTTTGCTGAGAGCTCTTCCA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; SEQ ID NO 31450; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                     Page 616; 673pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                               2000WO-IB00403.
                                                                                                                                                                                                                          Bougueleret L,
                                                                                                                                                                                                                                                                                             99US-0126269
99US-0131961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.2%;
                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.8;
Pred. No. 2e
                                                                                                                                                                                                                           Chumakov I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23;
                                                                                                                                                                                                                           Cohen-Akenine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ST
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RESULT 7
AAH51581/c
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CC marker containing sequences are related are involved in drug metabolism.

CC Sequences AAH51594 - AAH51598 represent the genomic sequence of the CC MGSTII gene and four alternative MGSTII cDNA sequences. AAB62905-AAB62906 CC are MGSTII gene products. PCR priners AAH51599 and AAH51600 are used in CC an example for the amplification of human genomic DNA fragments. The CC invention includes a method of genotyping comprising determining the CC identity of a nucleotide at a DME- or MGSTII-related biallelic marker in CC population of an allele of a DME- or MGSTII-related biallelic marker and CC population of an allele of a DME- or MGST-II related biallelic marker and CC population of an individual for inclusion in a clinical trial of a drug CC treatment. The method is also used to detect association between allele and phenotype, and to detect association between haplotype and phenotype. CC The polynucleotides are used, in hybridization assays, sequencing assays or allele specific amplification assays. The method can be used to determine whether an individual suffers or is at risk of developing assays or is at risk of developing assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma-glutamyltransferase 5 (GGT5), dipeptidase (DP), glucose 6-phosphate dehydrogenase (GGDH), phosphogluconate dehydrogenase (PGDH), and uridine diphosphate glucoronosyl transferases (UGT2). Bach of these sequences contains a biallelic marker/polymorphism, which is represented in the sequence as a degenerate/undefined base. The genes to which the biallelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; biallelic marker; single nucleotide polymorphism; SNP; MGSTII; microsomal glutathione S-transferase II; malate decarboxylase enzyme; DME1; ME1; cytochrome P450; glutathione reductase; GSHR; GSHS; GGT5;
                                                                                                                                                                                                                                                                                                                                                                                                                                   flavin-containing monooxygenase; FMO; gamma-glutamyltransferase 5; dipeptidase; DP; glucose 6-phosphate dehydrogenase; G6PDH; haplotype; phosphogluconate dehydrogenase; PGDH; drug metabolism; phenotype;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human MGSTII related DNA containing a biallelic polymorphism SEQ ID 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH51581 standard; DNA; 1000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                   WPI; 2000-638353/61
                                                                                                           Blumenfeld M,
                                                                                                                                                                                    25-MAR-1999;
30-APR-1999;
                                                                                                                                                                                                                                            24-MAR-2000; 2000WO-IB00403
                                                                                                                                                                                                                                                                                    05-OCT-2000
                                                                                                                                                                                                                                                                                                                        WO200058508-A2
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                               (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                 uridine diphosphate glucoronosyl transferase; UGT2; asthma; hepatoxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   614 TITCTITGCTCAGAGCTCTCC 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TITCTTTGCTGAGAGCTCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      756 BP; 224 A; 140 C; 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                         Bougueleret L,
                                                                                                                                                                                    99US-0126269.
99US-0131961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.2%;
90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.8;
Pred. No. 2
                                                                                                             Chumakov I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G; 213 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2e+02;
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                                                                                                             Cohen-Akenine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Polynucleotides comprising sequences from malate decarboxylase enzyme-related biallelic markers used for genotyping -

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CC dehydrogenase (GEPDH), phosphogluconate dehydrogenase (PGDH), and uridine CC diphosphate glucoronosyl transferases (UGT2). Each of these sequences CC contains a biallelic marker/polymorphism, which is represented in the CC sequence as a degenerate/undefined base. The genes to which the biallelic marker containing sequences are related are involved in drug metabolism. CC Sequences AAH51598 represent the genomic sequence of the CC MGSTII gene and four alternative MGSTII CDNA sequences. AAB52905 -AAB62905 (CC are MGSTII gene products. PCR primers AAH51593 and AAH51600 are used in CC an example for the amplification of human genomic DNA fragments. The CC identity of a nucleotide at a DME- or MGSTII-related biallelic marker in CC select an individual for inclusion in a clinical trial of a drug CC to select an individual for inclusion in a clinical trial of a drug CC treatment. The method is also used to detect association between allele and phenotype, and to detect association between haplotype and phenotype. CC determine whether are used, in hybridization assays, sequencing assays of the method of developing hepatoxicity on treatment with
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08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; G protein-coupled receptor; nGPCR-x; ss; antiviral; analges; cytostatic; cardiant; antidiabetic; anoretic; hypotensive; hyperteintiparkinsonian; nootropic; neuroprotective; antidepressant; viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; metabolic disease; cardiovascular disease; type 2 diabetes; obesity; anorexia; hypotension; hypertension; myocardial infarction; atherosclerosis; Parkinson's disease; psychosis; neurological disorder; schizophrenia; migraine; major depression; anxiety; mental disorder;
                                                                                                                                                          08-MAR-2001; 2001WO-US07322
                                                                                                                                                                                                                          13-SEP-2001.
                                                                                                                                                                                                                                                                                          WO200166750-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS30820 standard; cDNA; 1000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA encoding G protein-coupled receptor nGPCR-2428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1000 BP; 300 A; 200 C; 211 G; 288 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences
biallelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biallelic markers. The sequences are related to various human genes including microsomal glutathione S-transferase II (MGSTII), malate decarboxylase enzyme (DMEJMEI), cytochrome P450, glutathione sequences (FMO), reductase/synthase (GSHR/GSHS), flavin-containing monooxygenases (FMO), gamma-glutamyltransferase 5 (GGTS), dipeptidase (DP), glucose 6-phosphate chi-dronocom from the containing monooxygenases (FMO), symma-glutamyltransferase 5 (GGTS), dipeptidase (DP), glucose 6-phosphate chi-dronocom from the containing monooxygenase (FMO), symma-glutamyltransferase 5 (GGTS), dipeptidase (DP), glucose 6-phosphate chi-dronocom from the containing monooxygenase (FMO), symma-glutamyltransferase II (MGSTII), dipeptidase (DP), glucose 6-phosphate chi-dronocom from the containing monooxygenase (FMO), dipeptidase (DP), glucose 6-phosphate chi-dronocom from the containing monooxygenase (FMO), dipeptidase (DP), glucose 6-phosphate chi-dronocom from the chi-dronocom fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 641; 673pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TTTCTTTGCTGAGAGCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTCTTTGCTCAGAGCTCTCC 831
                                                                                                                                                                                                                                                                                                                                                                                                        depression; dyskinesia; Huntington's disease; Tourette's Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH51110-AAH51593 represent human DNA fragments which contain
2000US-0187581.
2000US-0187582.
2000US-0187714.
2000US-0187715.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.8; DB 21;
Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypertensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analgesic
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RESULT 9
AAV59153
    В
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                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            conditions such as infections, such as viral infections caused by HIV-1 (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, ancrexia, hypotension, hypertension, myocardial infarction, atherosclerosis), Parkinson's disease, and psychotic and neurological disorders, including schizophrenia, migraine, major depression, anxiety, mental disorder, manta depression, and dyskinesias, such as Huntington's disease or Tourette's Syndrome and many other diseases and syndromes listed in the specification. nGCCR-x polynucleotides and syndromes listed in the specification modulators, may also be used in diagnostic assays for such diseases or conditions. The present sequence encodes a G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
                                                                         Homo sapiens.
                                                                                                                    ss; human;
                                                                                                                                             Human ReprosA-1 coding sequence
                                                                                                                                                                             14-DEC-1998
                                                                                                                                                                                                                                   AAV59153 standard; cDNA; 2573 BP
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1000 BP; 265 A; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G protein-coupled receptors termed nGPCR-x nGPCR-x polynucleotides, polypeptides, and modulators may be used in the treatment of diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules encoding G protein-coupled receptors termed nGPCR-x, useful in the treatment and diagnosis of viral infections, cancers and mental disorders (e.g. Parkinson's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel isolated nucleic acid molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 221-222; 336pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      schizophrenia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAU19251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-536778/59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000;
08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000;
08-MAR-2000;
                                                                                                                                                                                                                                                                                                            791 TTTCTTTGCTCAGAGCTCTCC 771
                                                                                                     vitro fertilisation
                                                                                                                                                                                                                                                                                                                                    3 TTTCTTTGCTGAGAGCTCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                  ocal
                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                              Reprosa-1; contraceptive; anti-sperm; fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood LS;
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0187825.

2000US-0187828.

2000US-01877829.

2000US-0187839.

2000US-0187839.

2000US-0187874.

2000US-0187874.

2000US-0187874.

2000US-0187894.
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2000US-0187928.
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                              125..1654
/product= "ReproSA-1 protein'
                /*tag=
                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               71.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                 Score 17.8;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          299 G;
                                                                                                                                                                                                                                                                                                                                                                                                                         228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                               2.1e+02
                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                             Length 1000;
                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 10
ABL26658
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The ReproSA-1 polypeptide, it's fragments, or nucleic acid encoding them are used in contraceptive vaccines to generate an anti-sperm response. Antibodies can also be used as topical contraceptive (spermicide), also antisense sequences, ribozymes and triplex-forming molecules. Detection, by reaction with immobilised peptides, of anti-(I) antibodies (in serum, semen, saliva, cervical or vaginal mucosa) is used to diagnose immunological infertility and to monitor the effect of vaccination. nucleotide fragments are used to diagnose infertility-associated mutations in the gene encoding Repro-SA, and for isolation of related sequences. Peptides and anti-idiotypic antibodies against the antibodies are used to inactivate the antibodies i.e. to increase fertility and may be added to sperm samples before in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sperm-specific polypeptide ReproSA-1 and related nucleic acid transformed cells and antibodies, useful in contraceptive vaccines or compositions, and for diagnosis and treatment of infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              French CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2573 BP; 754 A; 532 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REPR-) REPROGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fertilisation.
                                     23-MAR-2000;
11-JUL-2000;
                                                                           23-MAR-2001;
                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                      pharmaceutical; gene;
                                                                                                                                                                                                     Drosophila;
                                                                                                                                                                                                                            Drosophila melanogaster genomic polynucleotide SEQ ID NO 31447.
                                                                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                                                                             ABL26658
           (PEKE ) PE CORP
                                                                                                       27-SEP-2001
                                                                                                                                   WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                              252 TGTCTTTGCTGAGAACTCTTC 272
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity les 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            TTTCTTTGCTGAGAGCTCTTC
                                                                                                                                                                                                                                                                                                               standard; DNA; 3153 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neilson LI,
                                                                                                                                                                                                    developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                         (first entry)
                                     2000US-191637P.
2000US-0614150.
                                                                              2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0039574
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                                                                                                                                                                                                                                                                                                                                                                                                                                              71.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.8;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        586 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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RESULT 11
ABL26632
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG511), expressed DNA sequences (ABLIG175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1746 TCTTTCCTGAGCGCTCTTCCA 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3153 BP; 864 A; 693 C; 665 G; 931 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 31447; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide SEQ ID NO 31369.
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                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                         Drosophila; deve pharmaceutical;
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                                                                Claim
                                                                                                                                              WPI; 2001-656860/75
                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231
                                                                                           interactions
                                                                                                                                                                                                (PEKE ) PE CORP NY.
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                                                               1; SEQ ID NO 31369; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                    developmental biology; cell signalling;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                          gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.8;
Pred. No. 2
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                                                                                                                                                                          Myers EW;
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                                                                                                          and cell-cell
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of

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RESULT 12
AAD31629
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                                                                                                                                                                 Query Match
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  6994
                                                                                                                                                                                                                                                                                         The invention relates to a polypeptide having GT1209, GT1354 or GT0946 activity obtained from Arabidopsis. The invention may also be applied to the development of herbicide tolerant plants, plant tissues, plant seeds and plant cells. The polypeptide is useful as herbicide targets in screening assays to identify potential herbicides and inhibitors of GT1209, GT1354 or GT0946 scrivity. A compound having herbicidal activity is useful for suppressing the growth of a plant. The newly discovered GT1209, GT1354 or GT0946 genes are essential for seeding growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide having GT1209, GT1354 or GT0946 activity, obtained Arabidopsis, useful as herbicide targets in screening assays to identify the inhibitors or potential herbicides -
                                                                                                                                                                                                                Sequence 8002 BP; 2119 A; 1489 C; 1502 G; 2892 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 72-74; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levin JZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000; 2000US-222779P
                                                                                                                                                                                                                                                                          development. The present sequence is Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-2001; 2001WO-EP08910.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GT1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana GT1209 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL1040-ABL16175) and the encoded proteins (ABBD18737-ABB72072).
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                                                                                                                                         Local
                             2 CTTTCTTTGCTGAGAGCTCTT 22
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CTTTCTTTGCTGATTGCTCTT 7014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; herbicide; plant tissue; cell; seedling growth; development;
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19; Conserv
                                                                                                                                         Similarity
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                                                                                                            Conservative
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                                                                                                                                 71.2%;
90.5%;
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                                                                                                                              Score 17.8; DB:
Pred. No. 3e+02;
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                                                                                                            Mismatches
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                                                                                                                                                              DB 24;
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                                                                                                                                                                                                                                                                          thaliana
                                                                                                                                                                                                                                                                        seedling growth and thaliana GT1209 gen
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                                                                                                                                                           Length 8002;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                             15-MAY-2002 (first entry)
                                                                                                                  ABL69358;
                                                                                                                                                                ABL69358 standard; DNA; 342 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression and secretion vectors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-OCT-2000
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                                                                                                                                                                                                                                                                                     152 GCCTTCTTTGCAGAGATTTCTTCC 129
                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                1 GCTTTCTTTGCTGAGAGCTCTTCC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5' EST; expressed sequence tag;
herapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 BP; 77 A; 38 C; 53 G; 54 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST,
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.6;
                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO: 12024.
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                223;
                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Prostate cancer related gene sequence SEQ

ID NO:7695

Human;

colon;

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18-SEP-2000;
20-SEP-2000;
20-SEP-2000;
20-SEP-2000;
22-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
28-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-OCT-2000;
20-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change i expression of at least one gene (I) of a signature gene set, where (I)
                                                                                                                                             screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2001; 2001WO-US10838.
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                                                                                                      Claim 1;
                                                                                                                                           determining
                                                                                                                                                                                                                            WPI; 2002-188264/24.
                                                                                                                                                                                                                                                                                                                              (AVAL-) AVALON PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                    SEQ ID 7695; 44pp; English.
                                                                                                                                                                                                                                                                  Augustus M, Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-237295P.
2000US-237316P.
2000US-237425P.
2000US-237598P.
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2000US-237606P.
                                                                                                                                                                                                                                                                                                                                                                         2000US-245084P
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2000US-237294P.
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                                                                                                                                        change in
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te; pancreas; carcinoma; antitumour; cancero
                                                                                                                                                                                                                                                                                          Carter
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                                                                                                                                                                                                                                                                                          Ebner R,
                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, ossophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
                                                                                                                                                                                                                                                                                                                                             25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate expression marker cDNA 11060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 342 BP; 36 A; 109 C; 92 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                               Claim 1; Page 1792; 11750pp; English.
                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV11069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV11069 standard; cDNA;
                                                                                                                                                                                                                                                                                Schlegel R,
                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-2000;
16-MAR-2000;
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                                                                                                                                                                                                                                               2001-662795/76.
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20; Conser
                                                                                                                                                                                                                                                                                                                                             2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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                                                                                                                                                                              presence of prostate cancer, stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.4%;
83.3%;
                                                                                                                                                                                                                                                                                 Monahan JE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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patient;

the efficacy of a therapy for inhibiting prostate cancer

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CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.

SQ Sequence 384 BP; 139 A; 87 C; 73 G; 85 T; 0 other;
SQ Sequence 384 BP; 139 A; 87 C; 73 G; 85 T; 0 other;

Query Match
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CTTCTTTGCTGAGAGCTCTTCA 25
Db 374 CTTTCTTTGCTGAGAGCTATTTCA 351

Search completed: March 17, 2003, 10:50:50

Search completed: March 17, 2003, 10:50:50
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-836-439-5
25
1 gctttctttgctgagagctcttcca 25
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(without alignments)
458.154 Million cell updates/sec
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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93.6	93.6	93.6	93.0	2 1	93.6	93.6		Match	Query	œ	
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BI730233	BG403992	BI736587	BI734160	D1/0/039	BT737600	BE950666		ID		SUMMARIES	
BI730233 603350201	BG403992 602419859	BI736587 603361053	BI734160 603351436	B1/3/699 603358627	######################################	RE950666 III-M-CEO-	• • • • • • • • • • • • • • • • • • • •	Description			

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3836	6205	3439	3854	2197	9320	3298	3791	3956	3926	3791	9361	17212	12998	10422	13227	13456	73636	26152	37245	2973	29384	2982	3732	1046	73060	2941:	7344	7380,	9371	7356	2981	7370	2958	7350	7369	BG298553	7296	7301
BI738365 60	262056 6	734393 6	938546	921973 /	293203 6	932985	737919	739561	739285	737918	293614 6	872123	729984	404226	732279	734568	1736361	3261526	1872453	3297332	3293849	3298242	1873234	3404627	1730669	3294123	1734477	1738044	11756W	1735675	3298167	1737008	G295809	1735044	1736996	G298553	1729678	1730180
03361127	237389	335114	ENCOUR	ENCOME	5100EC	ENCOME	27777	336181	335957	335749	239027)339643	200255	1242026)33542(335640	0336007	023732	033980	023954	0239036	239630	033975	024207	033503	0239091	111111	7.5.5.0	- K - C - C - C - C - C - C - C - C - C	865550	023963	033608	22020	033561	033608	023969	033493	033497

ALIGNMENTS

	COMMENT	JOURNAL MEDLINE	TITLE	AUTHORS	REFERENCE	CHORMATON	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	RESULT 1 BE950666/c
National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA Tel: 301 443 1706 Fax: 301 443 9890 Email: mESTemail.nih.gov The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site	Contact: Chin, H	Genome Res. 6 (9), 791-806 (1996) 97044477	Normalization and subtraction: two approaches to facilitate gene discovery	Bonaldo, M.F., Lennon, G. and Soares, M.B.	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 402)	Eukaryota; Metazoa; Chordata; Craniata, Vertehrata, Eutological.	house mouse.	EST.	BE950666.1 GI:10589332	UI-M-CEO-aza-d-06-0-UI 3', mRNA sequence. BE950666	402 bp mRNA linear EST 29-APR-2002 UI-M-CEO-aza-d-06-0-UI.sl NIH_BMAP_Ret3 Mus musculus cDNA clone)))

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RESULT 2
B1737699
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
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                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/strain="C57BL/6J"
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NIH-MGC http://mgc.n.inih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/lab_host="0H10B (phage-resistant)"
/lab_host="0H10B (phage-resistant)"
/note="0rgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="0rgan: eye; Vector: pcMV-SPORT6; Site_1: NotI;
/note="0rgan: eye; Vector: pcMV-SPORT6; Site_1: Note-
site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 636)
                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 649)
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Location/Qualifiers
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11936 row: j column: 13
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Tissue Procurement: The Cepko Laboratory
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                    Tissue Procurement: The Cepko Laboratory
                                    Email: cgapbs-r@mail.nih.gov
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cDNA Library Preparation: Life Technologies, Inc
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/clone="IMAGE:5368044"
/clone_lib="NIH_MGC_94"
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10435 row: e column: 15
High quality sequence stop: 644.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Plate: LLAM11909 row: b column:
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/Clone="IMAND: JOJA".
/Clone="Libe"NIH_MGC_94"
/tlssue_type="retina"
/tlsue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCrw-SPORT6; Site_1: Not1;
/note="Organ: eye; Vector: pCrw-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-spORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 203 c 140 g 142 t
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/clone="IMAGE:4526966"
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/clone="IMAGE:5357472"
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                                                                                                                                                                                                      GCTTTCTTTGCTAAGAGCTCTTCCA 426
                                                                                       BI729678 663 bp mRNA linear EST ZV-SEF-Z 603349362F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5356959 5',
                                                                                                                                                                                                                                                                        24;
                                                BI729678.1 GI:15706691
                                                                  BI729678
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11908 row: p column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
Mus musculus
                 house mouse
                                                                                mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: LLAM11908 row: p column: 06 High quality sequence stop: 649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5357429"
/clone_lib="NIH_MGC_94"
/tissue_type="rettina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pctW-SPORT6; Site_1: Not1;
Site_2: Sali, Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
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Pred. No. 24;
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Pred. No. 24;
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                                                                                                      DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10395 row: i column: 10
                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BG298553
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
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                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 672)
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                                                                                   e: LLAM10395 row: i column: quality sequence stop: 666.
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//db_xref="taxon:10090"
//db_xref="taxon:10090"
//clone="IMAGE:5356959"
//clone_lib="NIH_MGC_94"
//tissue_type="retina"
//tab_host="DH10B (phage-resistant)"
//note="Organ: eye, Vector: pCMV-SPORT6; Site_1: NotI;
//note="Organ: eye, Vector: pCMV-SPORT6; Site_1: NotI;
//site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/organism="Mus musculus"
/db_xref="taxon:10090"
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96.0%;
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Rodentia;
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Pred. No. 24;
0; Mismatches
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TITLE
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    409
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GCTTTCTTTGCTAAGAGCTCTTCCA 433
                                       GCTTTCTTTGCTGAGAGCTCTTCCA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 676)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence
BI736996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11936 row: c column: 12
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                                                                                   Conservative
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                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5367875"
/clone=1ib="NIH_MGC_94"
/tissue_type="retina"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
44 a 214 c 160 g 158 t
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/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

a 206 c 156 g 160 t
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Pred. No. 24;
                                                                                                    Score 23.4;
Pred. No. 24
                                                                                   Mismatches
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VERSION
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BG295809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTTTCTTTGCTGAGAGCTCTTCCA 25
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Libzary Preparation: Life Technologies, Inc.
cDNA Libzary Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 682)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                              BG295809 682 bp mRNA LINEBT EST 41-FEB-4 602393292F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4505134 5',
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Tissue Procurement: The Cepko Laboratory
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BI735044
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603356176F1 NIH_MGC_94 Mus musculus
                                                                                      Contact: Robert Strausberg, Ph.D
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National Institutes of Health, Mammalian
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Plate: LLAM11924 row: h column:
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/clone="lnAGE:536395"
/clone=lib="NHLMGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resigtant)"
/lab_host="DI910B (phage-resigtant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
52 a 220 c 156 g 152 t 1 others
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BI737008
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10378 row: g column: 23
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Location/Qualifiers
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Plate: LLAM11936 row:
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                /tissue_type="retina"
/lab_host="DB10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."

a 216 c 156 g 165 t
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/dlone="IMAGE:4505134"
/clone=1b="NHHMGC_94"
/clone_lib="NHHMGC_94"
/fissue_type="rethia"
/fissue_type="rethia"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
                                                                                                                                                                                                         /clone="IMAGE:5368117"
/clone_lib="NIH_MGC_94"
                                                                                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
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205 c 167 g 173 t
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96.0%;
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Pred. No. 24;
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RESULT 15
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                                                                                                               BI735675
603357821F1 NIH_MGC_94 Mus
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BI735675
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                Mus musculus
                                                                    BI735675.1 GI:15712688
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10385 row: h column: 01 High quality sequence stop: 677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
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Mammalia; Eutheria; Rodentia;
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/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 %b. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 218 c 164 g 166 t
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/tissue_type="retina"
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/db_xref="taxon:10090"
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Best Local Similarity 96.0
Matches 24; Conservative
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RS NIH-MGC http://mgc.ncl.nih.gov/.
RI Unpublished (1999)
Lontact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 697.
Location/Qualifiers
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High quality sequence stop: 697.
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//db_xref="taxon:10090"
//clone=_Ibx=ni=_10090"
//clone__ib="Nail_MGC_94"
//clone__ib="Nail_MGC_94"
//tlssue_type="refina"
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Match 5 317515 5 10243 5 10467 5 152556 5 152556 5 158633 3 178199 3 224068 9 907 9 3159 9 57507 9 107628 111984 111984 117628 178168 180970 182152 189281 189281 191434 197437 223761 229247 17938 42208 116685 Length DB) ACO9888 ACO99415 AED11043 AED10860 CNSO1DSY ACO19027 ACO11263 ACO15472 ACO15472 ACO15473 ACO15473 ACO15473 ACO15473 ACO15473 ACO15473 ACO15473 ACO15473 ACO15473 AC105316 AC0971864 AC097186 AC097180 AC1513347 AC093902 AC1097610 AC111144 AC125751 AC121805 AC117841 AC100433 AL589989 HS516C23 AC012350 AC09302 AC067929 AC012458 AC087477 AL772303 AC127239 HSDYSE51 AL603652 AC097448 AC013491 SUMMARIES 293021 Human DNA S AC012350 Homo sapi AC009302 Homo sapi AC009302 Homo sapi AC0087477 Homo sapi AC0087477 Homo sapi AC0127239 Mus muscu AC098888 Mus muscu AC098415 Mus muscu AC098415 Mus muscu AC019027 Homo sapi AC011263 Homo sapi AC011263 Homo sapi AC011263 Homo sapi AC011272 Homo sapi AC011272 Homo sapi AC011272 Homo sapi AC011274 Homo sapi AC011274 Homo sapi AC011275 Homo sapi AC01271 Homo sapi AC01271 ACD01341 Homo sapi AC01341 Homo sapi AC010511 ACD01341 Homo sapi AC010511 ACD01341 Homo sapi AC010513 Homo sapi AC010513 ACD01341 Homo sapi AC010513 ACD01341 Homo sapi AC010513 ACD01341 Homo sapi AC010513 ACD01341 Homo sapi AC010514 Homo sapi AC011805 Mus muscu AC1160314 Homo sapi AC117941 Rattus no AC117941 Rattus no AL160314 Homo sapi AC117941 Rattus no AF198437 Theileria AL589989 Human DNA Description

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ALIGNMENTS

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REFERENCE	SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION		DEFINITION	LOCUS	AF198437	RESULT 1
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae; Theileria. 1 (bases 17114 to 17938)	Theileria parva. Theileria parva	AF198437.1 GI:11545211	AF198437 L36964	20 protein 3, hypothetical telomeric SfII fragment 20 protein 2, and hypothetical telomeric SfII fragment 20 protein 2, complete cds.	a parva strain Muquqa hypothetical	AF198437 17938 bp DNA 11page TNV 05-D50-2000		

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-CCT-1999) Unit 5, International Livestock Research Institute (ILRI), Old Naivasha Road, Nairobi P.O. Box 30709, Keny On Dec 5, 2000 this sequence version replaced gi:624245.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic open reading frames encoding secretory proteins are located less than 3 kilobases from Theileria parva telomeres and. Biochem. Parasitol. 110 (2), 359-371 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sohanpal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bishop, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-JAN-1995) Unit 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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4 (bases 1 to 17938)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 17114 to 17938)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 17938)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTPTTYTTKSDPTTTATATETSSSTLTTESDTATTQTTPVTTPTSSGSSVTQSKRLES
SSTSGNIHTFTSGVSHSAVDASQGASVLDSGSSSSTLVLTEYKRLPSIRLTTSTDTDT
SSKSQTATPVTTTTNVALDIDKKQSTDQFEYSDINNYRLYVAKTNFVFNKIVQGTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt STTPKSQNQTQSSQSQSESTASATSRRRTGTTGAQGSQPTKPPSQPASSNGSGSHASP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical telomeric SfiI fragment 20 protein _{3}^{\mathrm{m}}
                                                                                                                                                                                                                                                                                                                       VEGNETYSHOCKCHTYATAGEGNTEGKYNKGTRYVWEPVGNVQAKKIIYVDDHYKNVV
VYLTDCKFLLLKQSDNNWDDVTKYTLDVSKLVFLGDNHGATSLGVSASVTVVDTAMTL
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PQVSGPAVTPSTATPSPAKVTSPPAATLSGTEVTPPKVAVSGTPVTLDIDNTQSASEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYGEGDRLLKSYDYSVTLSCLAFSYEFNVGSECHKVKYGDDVLWNHSDDSOFGTIKTF
SLDLPKNOFTIKNNSGTVKNVEFKYVILDLNTMESTDHFDRTGDDGIFKFVVKSGYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLAKNYFFYKNSADIYKKLELKY ISLDIDKKQSTDESDYSKSDCHTYMTKSNFYFNRI
VQGTDFYWKSQYLFGTKYTAAGDFLTILLNNGTFKLFQKSYCEWIDITPNKHDIGKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IWESKDYCATSVTTKTIDNKVFLAIVLSNGMFTLVEKSSGKWTDITLIGTWYLHLKFY
GDRDTEIKSSKYSVTMSGLSYNLDFNTNVDCKKIKYNNVTLWSHTDDSEFGTIKSLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RASTGQSSTPKSQPTTPTSQSQPKSTASRTSSTGVGQARGTPSSATSQPSRGVGVGRG
SQPKATAATIGTSTPTTPPTPTTSAAQTKATPTTGARPATQPKVTPASASSTQPKSQA
NVTPVSGSAAPSVSTSATPTKPVSQSTPTTSVTKVTLNIDTTKESTSELDYSKIGDIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Theileria parva"
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                                                                                                  CKKITLDNYTLWSHTDDTQFGTIKSFSLGLVLNGFFIKNESGTVKPAEPTKVTLDIEK
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EFDISYIEGSDHIYIPKENRVFNKVVRGPTLIWESKDNVCATIVTISSKFLSILFDNN
                                                                                                                                                                                                                                                       FEQSEGNWIDITDKRHNLTKLKFFNDSNAQIKPTEYTVTIVELSYRIQFSQGTICRKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STSYNVTRLKFLIDDNSELSTSDYKVTVAEHCYNLEFNSDVKCSKITHNGADLWKHSD
DTQFGTIKSLHLNLINNQLGLKNQSNTLKELQAPLPPTPDVTDTTGTKITIDLNETKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKVVQGTSVVWEPRDSAYCTEVTYIVAGDFKYLSAVLDNGSCLLLYKTSKDKPFKDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VWKHSDDTDFGSIKSLFIDLISNQLSVKNESGQLKKLEYKPKESNGTTSETADATKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWTDVTKERYDVDKLKFFGENDAALNKSSYSTTLISYSYSLEFNAGVKCQKVKYGNED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYTPKQNHLFSKVTHGSVVVWESKTEVHGTRVTYVCIIKYLVVLLSNDMFLLFHQSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MRKCMIFIKLLFYIALLHKWNGVESQPTSSGRSNSSGSQGSRAQ/
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                                                                                                                                                                  TFKLFQESEKQWTDITSDRHNVASLKFYGDNNVEIKLSDYIVSMSGLSYNFEFKTGVK
                                                                                                                                                                                                                                                                                                   DYKDEGGVVTYTPKENHVFSKVTEGPIVLWKSDDVSGTMVRICSKLLVILFNNNEFKL
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                                                                   INLSNGTTKEFQQSDSKWTESQTSSPVTTSSSSAQTATTETATTGTTTTKTVLDIDI
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Query Match

88.2%;

Score 19.4;

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ECKEKNOVTSYTAKSDLVFTK ITHKTTVVWESGGNVCAILVSVKAEFLAILLSNNQFK
LFQKSSDGTWKDITSQRHNISNLKFLGQGGSVLKSPDYSVSMSGLILVYEFNTKCTKI
MLENENIWKPDDDPKFPKIKSLSLDIASNKFSLKSDTAVKELELSLATSTESATKSAT
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TTORLLLTRGQSTTDVIEAVDVRPITLDLTTATNNKFSRTDKDGYVTYTANPGFVFGK
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YLFTKVTEGAKVVWESNDTVGGTLVTTTGEFLAILLNNLFKLFLKSSEWEDITKSRI
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                                                                                                                                                                                                                                                                                                                           FTEKAGVNCKRINYGDVVIWTHTDDKFEYITNFDLDLVKNEFFVFDDKRKSRKVNYEG
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DYSKTDNVHVYTAKSNHSFSKITRGSNTVWEAPDNVSAKSVIFVDESIKYVTIDLGGG
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2"
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PPPPYSESQHDTPETPSYPPPPYSESQHDTPEPPSYPPPPYSESQHEAPQ
                                                                                       SDDTDFGY1KSLLIDLVANKFRVKNDSGQLKKLDFKPSTPRL1P1PEQQYQQAPPQSR
PTPTYPRPP1PARPPYPSHQLPVQPQP1HPGPQLSVRQPVRPPAYSE1QYDTPETPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAG37802.1"
/db_xref="GI:11545214"
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP http://www.second.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
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                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone RP1-11688 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP11-13J16 is at 42109 in this sequence. The true right end of clone RP3-483L3 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
http://www.sanger.ac.uk/HGP/Chr6
RPI-116B8 1s from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On May 15, 2001 this sequence version replaced gi:13751581. During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 42208)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECTOR: PCYPAC:
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                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
  3125. .3190
/note="33 copies 2 mer ca 66% conserved"
                                                                                                                /note="MIR repeat: matches 156. .262 of consensus"
                                                                                                                                                                             /note="MLT1B repeat: matches 1. .383 of consensus"
                                                                                                                                                                                                                                                                       /clone="RP1-116B8"
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                             clone_lib="RPCI-1"
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ne 6, complete
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                                                                                                                   /note="MER5B repeat: matches 3. .173 of consensus" 25110. .25213
/note="L2 repeat: matches 2482. .2626 of consensus" 26454. .26782
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17136. .17192
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/note="Aluy repeat: matches 1. .309 of consensus"
3996. .4294
                                                                                                                                                                                                                                                                                                    /note="L1PA13 repeat: matches 6063. .6156 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                            /note="FLAM_A repeat: matches 1. .130 of consensus"
                                                                                                                                                                                              note MLT1A1 repeat: matches 44. ,315 of consensus"
                                                                                                                                                                                                                                                     'note="36 copies 2 mer at 65% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="L2 repeat: matches 1246. .1462 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1MB3 repeat: matches 5434, .6176 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L2 repeat: matches 2158. .2302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1MA4A repeat: matches 5717. .6288 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="LTR18B repeat: matches 1. .603 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat: matches 1. .301 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MIR repeat: matches 13. .148 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MER63A repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1MA9 repeat: matches 6087. .6270 of consensus"
                                                         "MIR repeat: matches 51. .157 of consensus" .26447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 22356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 152.
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                                                                                                                                                                                                                                                                                                                                                             repeat: matches 3. .152 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2459 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .201 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .37 of consensus"
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RESULT 3
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                                                                                                                                                                                                                                                                                                                             HS516C23 116685 bp DNA linear Human DNA sequence from clone 516C23 on chromosome repeat (D6S402) and GSSs, complete sequence.
requests: clonerequest@sanger.ac.uk

On Mar 29, 1999 this sequence version replaced gi:3821035.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
                                                                               Submitted (23-MAR-1999) Sanger Centre, Hinxton, Cambridgeshire CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 116685)
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                             Direct Submission
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/note="MEB67A repeat: matches 1. .542 of consensus" 28802. .28943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /11840. .41963
/note-"LTR16C repeat: matches 259. .387 of consensus"
9645 c 9179 g 11128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 23. 35717. .35886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33104. .33456
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/note-"MIR repeat: matches 126. .190 of consensus"
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consensus"
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30888. .31049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MSTD repeat: matches 1. .394 of consensus"
34340. .34703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1MB1 repeat: matches 5782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="MIR repeat: matches 66. .147 of consensus"
39973. .41078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="19 copies 2 mer ac 100% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="L1MC/D repeat: matches 5395. .5756 of consensus"
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "LIM2 repeat: matches 4729. .5799 of consensus" .41153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .36728
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6q12 Contains CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence is the entire insert of clone 51623. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516C23 is from the library RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human chromosome 6, constructed by the Sanger Centre Chromosome
Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was generated from part of bacterial clone contigs human chromosome 6, constructed by the Sanger Centre Chromosome 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5223. .5418 /note="MLT2E repeat: matches 8. .201 of consensus" 5676. .5798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4135. .4260
/note="LIPA12 repeat: matches 534. .659 of consensus"
4359. .4701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="I
3221. .3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1MB8 repeat: matches 5015. .5445 of consensus"
9728. .10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1PA12 repeat: matches -1411. .-954 of consensus" 5223. .5418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="LIPA12 repeat: matches 131.
4135. .4260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3221. .3704
/note="L1PA12 repeat: matches 252.
3656. .4127
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L1MB8 repeat: matches 5467. .6169 of consensus" 10894. .12058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 166.
9021. .9292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="LTR16C repeat: matches 260. .387 of consensus"
7126. .7224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                        /note="L2 repeat: matches 1706. .1969 of consensus"
19219. .19457
                                                                                                                                                                                                                                  16400.
                                                                                                                                                                                                                                                                             14401
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1PA2 repeat: matches 4981. .6144 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MLT1A1 repeat: matches 1. .365 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="RPCI-3"
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                                          /note="MIR repeat: matches 9. .248 of consensus"
20472. .20676
                                                                                                                                        18906.
                                                                                                                                                        /note="L2 repeat: matches 2570. .2698 of consensus"
                                                                                                                                                                                                                                                     /note="MLT1B repeat: matches 1.
                                                                                                                                                                                                                                                                                              /note="15 copies 2 mer gt 100% conserved"
                                                                                                                                                                                                                                                                                                                                                note="L2 repeat: matches 2655. .2698 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                           note="25 copies 2 mer aa 78% conserved"
                                                                                                                                                                                                        'note="L2 repeat: matches 2657.
L2 repeat: matches 627. .842 of consensus" .21698
                                                                                                                                                                                     .16985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L1PA12 repeat: matches 751.
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                                                                                                                                        .19147
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                                                                                                                                                                                                                                16486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 2381. .2655 of consensus"
                                                                                                                                                                                                                                                        .390 of consensus"
                                                                                                                                                                                                             .2746 of consensus"
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                                                                                                                                                                                                                 41800. .41805
/note="IS2 transposable element excised from this
                                                                                                                               /note="MLT1J repeat: matches 56. .505 of consensus"
42267. .42627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSp/q repeat: matches 192. .276 of consensus" 33484. .33868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="22 copies 2 mer tt 75% conserved" 24361. .30507
              'note-"71 copies 2 mer tt 63% conserved"
                                                                                                                                                                                                                                                            11529. .41819
note="L2 repeat: matches 1780. .2071 of consensus"
                                                                                                                                                                                                                                                                                                         'note-"MIR repeat: matches 12. .120 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"L1M4 repeat: matches 3047. .3235 of consensus"
38463. .38837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1MC1 repeat: matches 5398. .6314 of consensus" 23343. .23754
                                                                                                       note="L2 repeat: matches 2301. .2677 of
                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1M4 repeat: matches 3790. .4186 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"Alusx repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note-"AluSq/x repeat: matches 1. .129 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="L1M4 repeat: matches 2359. .3033 of consensus"
37749. .37877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1ME2 repeat: matches 5476. .6154 of consensus" 6950. .37121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94220. .34364
(note="LTR33 repeat: matches 382. .517 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note-"LTR33 repeat: matches 1. .143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L2 repeat: matches 1862. .2267 of consensus"
33887. .34010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L2 repeat: matches 960.
31811. .32018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="23 copies 2 mer ca 100% conserved" 7928. .38256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L1MA4 repeat: matches 6176. .6290 of consensus" 5141. .35266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14403. .34964 .
note="LIMEC repeat: matches 272. .906 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MIR repeat: matches 39. .262 of consensus"
12300. .33151
"note="L1PB1 repeat: matches 5323. .6155 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note-"MLT1B repeat: matches 1. .170 of consensus"
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24302. .24345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L2 repeat: matches 2029. .2520 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ote="L1MEc repeat: matches 1782. .1975 of consensus" 125. .37741
                                                                                                                                                                                               ition"
                                                                                                                                                                                                                                                                                                                                                                             47. .39138
te="AluJo repeat: matches 12. .293 of consensus"
44. .39389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                te-"Alux repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37. .34218
.e="16 copies 2 mer aa 84% conserved"
                                   "44 copies 2 mer aa 69% conserved"
.43640
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.44158
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Fizhigh, W., Forrest, C., Funke, R., Gage, D., Galdgan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galgan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Klein, J., Hewland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morman, C. H., O'Connor, T., O'Donnell, P., Marrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC012350 178168 bp DNA linear HTG 01-APR-200 Homo sapiens clone RP11-16N9, WORKING DRAFT SEQUENCE, 16 unordered
                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                             Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-16N9
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 178168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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HTG; HTGS_PHASE1; HTGS_DRAFT
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/note="L2 repeat: matches 2180.
54942. .55097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 49. .210 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="14 copies 2 mer ac 100% conserved <52243. .>52703
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/note="AluSq_repeat: matches 3. .311 of consensus"
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/note="MLTID repeat: matches 5. .505 of consensus" 44686. .45053
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96. .54852
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Pred. No. 90;
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Insert size: 176668; sum-of-contigs
Quality coverage: 6.4 in Q20 bases; agarose-fp
Quality coverage: 6.2 in Q20 bases; sum-of-contigs
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/organism="Homo sapiens"
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Tomlinson,C., Wohldmann,P., Maupin,R. and Reitz,L.
The sequence of Homo sapiens BAC clone RP11-71J24
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 180970) Sulston, J.E. and Waterston, R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
Waterston, R.H.
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RP11-71J24.
                                                                                                                                                                                                                                                                                           The RPCI-II human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://www.resgen.com)
                                                                                                                                                                                        The clone sequenced to the left is RP11-350124; the clone sequenced to the right is RP11-296A19. Actual start of this clone is at base position 1 of RP11-71J24; actual end is at base position 180970 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence
                                                                                                                                                                                                                                                                NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Aug 28, 2000 this sequence version replaced g1:5732171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restriction digest
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Submitted (13-AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-AUG-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_NH0071J24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 180970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summary Statistics
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                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                              Location/Qualifiers
                 /clone_lib="RPCI-11"
                                   /clone="RP11-71J24"
                                                           /map-"2"
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31064
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30933
/rpt_family="MER2_type"
35611. .35898
                                                                                                                                                                                                            /rpt_family="ERVL" 31213. .31623
                                                                                                                                                                  31690
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24585
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23476
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22146
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20445
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20732. .21129
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19203
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9120. .9530
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11531. .11729
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11735. .1
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             Birren.B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Abraham,H., Boukhgalter,B., Brown,A., Burkett,G., Calingopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Gage,D., Cadagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Grand-Pierre,N., Grant,G., Honson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., McCarthy,M., McEwan,P., McGurk,A., McMernan,R., McMernan,P., McGurk,A., McMernan,R., McMernan,P., McGurk,A., McMernan,R., McMernan,R
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1 (bases 1 to 182152)
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Homo sapiens chromosome 6 clone RP11-403120 map 6, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 6, clone RP11-403120
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Similarity 90.9%;
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Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J
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37177. .37310
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39561. .39809
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44962. .45131
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campoplano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will
                                                                                                                                                                                                                                                   be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 4.8 in Q20 bases; agarose-fp Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; M77815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
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Insert size: 180452; sum-of-contigs
1 2222: contig of 2222 bp in length
2223 2322: gap of 100 bp
2323 3785: contig of 1463 bp in length
3786 3885: gap of 100 bp
3886 6753: contig of 2868 bp in length
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101335 101434: gap of 100 bp
101435 117630: contry of 16196 bp in length
117631 117730: gap of 100 bp
117731 118293: contry of 20563 bp in length
138294 138393: gap of 100 bp
138394 157841: contry of 19448 bp in length
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67142. .75921
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58336. .67041
                                                                                                 /note="assembly_fragment"
117731. .138293
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101435. .117630
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30341. .40123
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14638. .21177
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2323. .3785
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/db_xref="taxon:9606"
/chromosome="6"
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10137. .14537
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182152: contig of 24211 bp in length
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JOURNAL
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AUTHORS
TITLE
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SOURCE
ORGANISM
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AC012458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 152828 AACACTTCTGAGTAACAAACAA 152849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
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                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; 23%
Chemistry: Dye-primer ET; 77% of reads
Chemistry: Dye-terminator Big Dye; 23% of reads
Assembly program: Phrap; version 0,990319
Consensus quality: 183385 bases at least Q40
Consensus quality: 185502 bases at least Q30
Consensus quality: 185573 bases at least Q20
Insert size: 197000; agarose-fp
Insert size: 188381; sum-of-contigs
Quality coverage: 4.50 in Q20 bases; sum-of-contigs
Quality coverage: 4.71 in Q20 bases; sum-of-contigs
                                                                                                     * NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO Sapiens chromosome 15 clone RP11-522B15, WORKING DRAFT SEQUENCE, 10 unordered pleces.

AC012458 AC012458.4 GI:8570271

HTG; HTGS PHACET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission Submitted (27-0CT-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA USA Sequence version replaced g1:6850536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; 77%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: H_NH0522B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo. 1 (bases 1 to 189281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                       be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
      4604
4704
9762
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1 40355 c 40613 g 47868 t
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clone_end:T7
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157942. .182152
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90.9%; Pred. No. 85;
4603: contig of 4603 bp in length
4703: gap of unknown length
9761: contig of 5058 bp in length
9861: gap of unknown length
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RESULT 8
AC087477
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ORIGIN
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                                                               REFERENCE
                                                                                                                         SOURCE
                                                                                                                                                                        ACCESSION
                                                                                                                                         KEYWORDS
                                                                                                                                                       VERSION
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                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                          ORGANISM
                                              AUTHORS
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Homo sapiens chromosome 15, clone RP11-522B15
Unpublished
2 (bases 1 to 191434)
                                              Birren, B., Nusbaum, C.
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          Homo sapiens
                                                                                                                                                                      Homo sapiens chromosome 15, clone RP11-522B15, complete sequence. AC087477
                                                                                                                                                         AC087477.8
                                                          (bases 1 to 191434)
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117944
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35490
35590
51473
51573
65230
65330
89667
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18747
18847
27397
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89767. .117943
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/db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_name:Contig15"
39374 c 39106 g 55769 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-522B15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contigl4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="assembly_name:Contig12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_name:Contig11"
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                                                                                                                                                         GI:21844630
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                                                                                                                                                                                                                                                                                                                                                           85.5%;
90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9: gap of unknown length
2: contig of 15883 bp in length
2: gap of unknown length
9: contig of 13657 bp in length
9: gap of unknown length
6: contig of 24337 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 8885 bp in length
gap of unknown length
contig of 8550 bp in length
gap of unknown length
contig of 7993 bp in length
                                                                                                                                                                                                                                                                                                                                                           Score 18.8;
Pred. No. 85;
                                                and Lander, E
                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                            912 others
                                                                                                                                                                                                                                                                                                                                                                           Length 189281;
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AUTHORS
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AUTHORS
        COMMENT
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Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehocxky, J., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nayven, C.,
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Riebe, K., Ries, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leboczky, J., Levine, R., Lidu, G., MacChean, C., MacGonald, P., Marquis, N., Matthews, C., McCarthy, M., McDwan, P., MacGran, K., McPertan, R., McHerters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., McDwan, P., McKernan, K., McPetres, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Ribback, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Stongez, C., Spencer, B., Stange-Thomann, N., Stodjanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Strauss, N., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Tamber, T., Travis, N., Trigilio, J., Ye, W.J., Young, G., Zainoun, J., Tamber, L., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., Lakocque, K., Lamazares, R., Landers, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 191434)
Submitted (16-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 16, 2002 this sequence version replaced 91:20043143.
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Direct Submission
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Center clone name: 522_B_15
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/rpt_family="(TC)n"

/rpt_family="(TC)n"

/complement(14459. .14464)

/note="<30 qual SNGL region"

/note="<30 qual SNGL region"

/note="<30 qual SNGL region"
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                                                                                                                                       complement(20896
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                                                                                                                                                                                                                 complement(14475...14479)
/note="<30 qual SNGL region"
complement(14493...14498)
/note="<30 qual SNGL region"
                                                        /rpt_family-"(TATATG)n"
                                                                                                                                                                                      rpt_family="Alusq"
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/db_xref="taxon:9606"
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/clone_lib="RPCI-11 Human Male BAC"
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3. .21016)
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. .6308
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2. .10428
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. .13926
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                                                                                     ly="(CA)n"
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AUTHORS
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VERSION
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AL772303/c
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                                                      Submitted (12-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 14, 2002 this sequence version replaced g1:21540206.
                                                                                                                                                                                                                                                                           197437 bp DNA linear HTG 13-JUL-2002 Mus musculus chromosome 2 clone RP23-185P20, *** SEQUENCING IN PROGRESS ***, 6 unordered pleces.
                           Center: Wellcome Trust Sanger Institute
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 197437)
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Web site: http://www.sanger.ac.uk
                  Center code: SC
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                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                AL772303.3 GI:21748303
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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complement(31104, .31225)
/rpt_family=""AluSp"
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complement(31951, .31993)
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31242 . 31310
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24327. .24350
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complement(22988. .23113)
/rpt_family="L2"
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31437. .31741
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/rpt_family="AluSq"
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complement/accor
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complement/20770
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complement/porro
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24471. .24597
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17835. 27005
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6549. .26667
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                                              --- Genome Center
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AC127239 223761 bp DNA linear HTG 17-J
Mus musculus chromosome UNK clone RP24-381A23, WORKING DRAFT
                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: bM185P20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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46843 46942: gap of 100 bp
46943 51200: contig of 4258 bp in length
51201 51300: gap of 100 bp
51301 62621: contig of 11321 bp in length
62622 62721: gap of 100 bp
62722 92981: contig of 30260 bp in length
92982 93081: gap of 100 bp
93082 143175: contig of 50094 bp in length
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                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment:00782
fragment_chain:2"
143276. .197437
/note="assembly_fragment:00847"
a 40264 c 38730 g 57970 t
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/chromosome="2"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:2"
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90.9%;
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contig of 54162 k
                                                                                                                                                                                                                                                                                  Score 18.6;
                                                                                                                                                                                                                                                               Pred. No.
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                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                     DB 2; Length 197437;
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence the as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 221262 bases at least Q40 Consensus quality: 221869 bases at least Q30 consensus quality: 222233 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (17-UUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 223761) McPherson, J.D. and Waterston, R.H.
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McPherson, J.D. and Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: M_BB0381A23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
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6671
22738
22838
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                                              /note="assembly_name:Contig10"
6671. .22737
/note="assembly_name:Contig11" 22838. .48321
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                                                                                                                                         /db_xref="taxon:10090"
/chromosome="UNK"
                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                   /clone="RP24-381A23"
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216233: contig of 3794 bp in length
216333: gap of unknown length
223761: contig of 7428 bp in length.
                                                                                                                                                                                                                                                                                                                                  48421: gap of unknown length
118533: contig of 70112 bp in length
118633: gap of unknown length
212339: contig of 93706 bp in length
212439: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                               6570: contig of 6570 bp in length 6670: gap of unknown length 22737: contig of 16067 bp in length 22837: gap of unknown length 48321: contig of 25844 bp in length
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HTG 05-JUN-2002

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Best Local Similarity 90.9
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                           Matches
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Submitted (21-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Apr 3, 2002 this sequence version replaced gi:17105321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (03-APR-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 229247)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 299247)
1 (bases 1 to 299247)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center Center code: WUGSC
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Submitted (05-NOV-2001) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACUYBUBUB 229247 bp DNA linear Mus musculus clone RP23-122NB, complete sequence AC098888
                                                                                                                                                                                                                                                                     Center project name: M_BA0122N08
                                                                                                                                                                                                                                                                                         Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                    Web site:http://genome.wustl.edu/gsc/index.shtml
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McPherson, J.D. and Waterston, R.H.
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                           Conservative
                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-122N8"
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216334. .223761
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118634. .212339
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41598 c 40871 g 69263 t
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212440. .216233
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                                               90.98;
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                           0,:
                                          Score 18.8; DB 10;
Pred. No. 83;
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Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 293243 bases at least Q40
Consensus quality: 303369 bases at least Q30
Consensus quality: 309642 bases at least Q20
Insert size: 224000; agarose-fp
Insert size: 322378; sum-of-contigs
Quality coverage: 37.21 in Q20 bases; sum-of-contigs
Quality coverage: 37.21 in Q20 bases; sum-of-contigs
Quality coverage: 24.94 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (05-JUN-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA
On Jun 5, 2002 this sequence version replaced g1:20069750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus chromosome UNK clone RP23-122D8, WORKING DRAFT SEQUENCE, 56 unordered pieces.
AC099415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; 168
Sequencing vector: plasmid; 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 317515) McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-NOV-2001) Genome Sequencing Center, 4444 Forest Park
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McPherson, J.D. and Waterston, R.H.
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McPherson, J.D. and Wat
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               1211: contig of 1211 bp in length
1311: gap of unknown length
2357: contig of 1046 bp in length
2457: gap of unknown length
3574: contig of 1117 bp in length
3674: gap of unknown length
4817: contig of 1143 bp in length
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6015: contig of 1098 bp in length
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/db_xref="taxon:10090"
/chromosome="UNK"
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17313 . 18620
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98934:
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96704:
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2: contig of 2991 bp in length
2: gap of unknown length
8: contig of 1646 bp in length
8: contig of 1874 bp in length
2: contig of 2874 bp in length
2: contig of 2874 bp in length
2: contig of 3001 bp in length
9: contig of 3001 bp in length
9: contig of 4015 bp in length
9: qap of unknown length
9: qap of unknown length
4: contig of 4315 bp in length
4: contig of 6730 bp in length
4: contig of 10686 bp in length
0: contig of 10686 bp in length
0: qap of unknown length
0: contig of 107530 bp in length
0: qap of unknown length
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                                                                                                                                            Score 18.8; D
Pred. No. 81;
0; Mismatches
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of 2182
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                                                                                                                                                                              Length 317515;
                                                                                                                                                Indels
                                                                                                                                                0;
                                                                                                                                                Gaps
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gap of contig ga

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28551: 29863:

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contig gap of contig gap of contig

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KEYWORDS
SOURCE
ORGANISM
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AL. Genome Res. 12 (4), 532-542 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (20-MAR-2002) Center for Genome Research, Whitehead
Institute, Nine Cambridge Center, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B
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Methanosarcina acetivorans C2A
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome.
AE011043 AE010299
AE011043.1 GI:19917413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ∕organism="Methanosarcina acetivorans C2A"
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gene CDS

gene CDS

complement (7624.

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                             complement(7624. .7914)
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AWWAFDFVSNWARLNYQRWTRVDILPLQQKIETEEVQKTILQWDECCRGKSDLEARDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGKSVESDVLDLLKGIPEIEYNTPDEVTREIERLESQRTREYTRPEY"
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Methanosarcina acetivorans C2A
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
                                                                                                                                                                                                                                                                                                                              Submitted (20-MAR-2002) Center for Genome Research, Whitehead Institute, Nine Cambridge Center, Cambridge, MA 02141, USA
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FVLLSWIALFSTMNTVLVVMLGGSRIVYGMANSGSLPKILARVHQKLKTPWTAICGIA
FFSSLFVFLGDIATVANIANFWIFIVFFIVNISLIKLRYTDPERKRPFRVPVSIGRFP
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                                                                                                                                                                                        /organism="Methanosarcina acetivorans C2A"
                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Pred. No. 1.8e+02;
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LAHEFGLELPLKTFDELSRTTPHLISLRPGGNFMLHFDRAGGVEAVVQRLASKILLD
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                                                                                                                                                                                                                                                                                                                                                complement(6986. .7579)
/gene="mtxA"
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/note="MA1804"
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                             TITLE
                           AUTHORS
                                                           JOURNAL
                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                            ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 15256)

Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Earottler, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Levy, M., Eckenberg, R., Bruls, T., deberardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Weissenbach, J. Sequencing of the human chromosome 14
                   Genoscope.
                                                       Unpublished
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                         AL122035.6 GI:14330253
HTG; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                 CNSOIDSY
                                                                                                                                                                                                                                                                                                   from chromosome 14 of Homo sapiens (Human), complete sequence
                                                                                                                                                                                                                                                                                                                      CNSOLDSY 152556 bp DNA linear PRI 06-JUN-2001
Human chromosome 14 DNA sequence BAC C-2555016 of library CalTech-D
                                  (bases 1 to 152556)
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Pred. No. 1.8e+02;
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 Query Match
Best Local Similarity
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Submitted (06-JUN-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jun 8, 2001 this sequence version replaced g1:12001723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percentage of bases with a quality value >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Overall quality chart :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: Phrap; version 2.0 Quality coverage: 6.31x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                             44388 a
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Identified using the e-PCR software (G. Schuler)"
32591 c 33034 g 42543 t
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Score 18.4; DB 9;
Pred. No. 1.4e+02;
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Pocus

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GACTTCTGAGTAACAATCAA 22

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Db 29842 GACTTCTGAGTACCAATCAA 29861

Search completed: March 17, 2003, 11:38:09

Job time: 574.495 secs

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Database :
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Gapop 10.0 , Gapext 1.0
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(without alignments)
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

9876	0 4 U 4	ς ω 2 1	Result No.
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78.2 78.2 76.4 76.4			Query
7626 349980 461 21477	1353 513	48908 801 877	Query Match Length DB
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ABL07736 AAH68529 AAC57234 AAK66626	AAC50782 AAK54111	AAK82338 AAC42853 AAO03999	ID
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DNA encoding novel DNA encoding novel H. pylori secreted H. pylori secreted	DNA encoding novel Tobacco leaf antif DNA encoding novel DNA encoding novel DNA encoding novel DNA encoding novel	Human polynucleoti DNA encoding novel DNA encoding novel Human immune/haema	Human cardiovascul Rchd534 gene seque Nucleotide sequenc	Human nervous syst Human nervous syst Human immune/haema Human immune/haema Buchnera sp. genom Human Orax polynuc Human ovarian canc DNA encoding novel DNA encoding novel Human polynucleoti rchd534 gene diffe Human rchd534 gene cDNA sequenc Human rchd534 gene CDNA sequence Human rchd534 gene CDNA sequence CDNA sequence of r Human rchd534 cDNA	Human immune/haema Human TANGO 405 cD

ALIGNMENTS

AAK82338 ID AAK82338 standard; DNA; 48908 BP. XX AC AAK82338; XX DT 07-NOV-2001 (first entry) XX DE Human immune/haematopoietic antigen genomic companies.	DE Human immune/haematopoietic antigen genomic sequence	KW Human; immune; haematopoietic; immune/haematopoietic		OS Homo sapiens. XX	PN WO200157182-A2.	PD 09-AUG-2001. XX	PF 17-JAN-2001; 2001WO-US01354. XX	PR 31-JAN-2000; 2000US-0179065.	04-FEB-2000;	24-FEB-2000;	16-MAR-2000;		 18-APR-2000;		18-APR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000;
	oietic antigen genomic sequence SEQ ID NO:37150.		apy; vaccine; metastasis; ds.				101354.		.79065.	.79065. .80628.	79065. 80628. 84664.	79065. 80628. 84664. 88350.	 .80628. .80628. .84664. .86350. .86350. .86350. .86350.	80625 80628 80628 84664 86350 86350 86350 98123 98123	79065 80628 84664 84350 86350 86374 98776 99076 98123 98123 98123 98123

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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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14-SEP-2000;
14-SE
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14-AUG-2000;
14-AUG-2000;
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2000US-0216880.
2000US-0217487.
2000US-0217496.
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2000US-0225270.
2000US-0225447.
2000US-0225457.
2000US-0225757.
2000US-0225758.
2000US-02256279.
2000US-0226681.
2000US-0226868.
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2000US-0224519.
2000US-0225213.
2000US-0225214.
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2000US-0227009
2000US-0228924
2000US-0229287
2000US-0229343
2000US-0229345
2000US-0229345
2000US-0229519
2000US-0229519
2000US-0230437
2000US-0230438
2000US-0231242
2000US-0231242
2000US-0231242
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2000US-02314134
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2000US-0232400
2000US-0232401
2000US-0233063
2000US-0233063
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2000US-0234223
2000US-0234223
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2000US-02358834
2000US-02358834
2000US-0236837
2000US-0236837
2000US-02368367
2000US-02363637
2000US-02363637
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2000US-0232081.
2000US-0231968.
2000US-0232397.
2000US-0232398.
 2000US-0237038
2000US-0237039
2000US-0237040
2000US-0239935
2000US-0239937
2000US-0239937
2000US-0241221
2000US-0241785
2000US-0241785
2000US-0241787
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                                                                                                                                                                         2000US-0236802
2000US-0237037
              20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
06-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
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          AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
                                                                                                                                                                                                                                                                         WPI; 2001-483426/52.
                                                                                                                                                                      Disclosure;
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                                                                                                                                                                                                                                                                                                           CA,
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2000US-0241808
2000US-0244617
2000US-0246475
2000US-0246476
2000US-0246476
2000US-0246478
2000US-0246524
2000US-0246528
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2000US-0249218
2000US-0249218
2000US-0249264
2000US-0251856
2000US-0251856
2000US-0251988
2000US-0251988
2000US-0251989
2000US-0251989
                                                                                                                                                                                                                                                                                                           Barash SC,
                                                                                                                                                                    SEQ ID NO 37150; 3071pp + Sequence Listing; English.
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Best Local !
           23-APR-1999
23-APR-1999
28-APR-1999
30-APR-1999
30-APR-1999
04-MAY-1999
05-MAY-1999
06-MAY-1999
07-MAY-1999
11-MAY-1999
14-MAY-1999
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14-MAY-1999
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK59590 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                         25-FEB-1999;
                                                                                                                                                                                                                                                                                                                            25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                     metabolic pathway; promoter; termination sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3233 GACTTCTGAGTACCAATCAA 3252
                                                                                                                                                                                                                                                                                                                                                                                                             Hybridisation assay; genetic mapping; gene expression control, protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana DNA fragment SEQ ID NO: 37100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC42853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC42853 standard; DNA; 801 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48908 BP; 14764 A; 10631 C; 10740 G; 12773 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GACTTCTGAGTAACAATCAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                          2000EP-0301439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
         990S-0132407
990S-0132484
990S-0132485
99US-0132486
99US-0132486
99US-0134256
99US-0134256
99US-0134218
99US-013421
99US-013421
99US-0134370
99US-0134370
99US-0134370
99US-0134370
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99US-0128714
99US-0129845
99US-0130077
99US-0130079
99US-0130510
99US-0130510
99US-0131449
99US-0132048
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990S-0123180
990S-0123548
990S-01235788
990S-0126264
990S-0126785
990S-0127462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.6%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ed. No. 42;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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    21 JUL 1999
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24-JUN-1999
28-JUN-1999
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16-JUL-1999;
19-JUL-1999;
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24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
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17-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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15-JUL-1999;
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01-JUL-1999
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16-JUN-1999;
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99US-0139462

99US-0139463

99US-0139750

99US-0139750

99US-0140695

99US-0140695

99US-0141287

99US-0142055

99US-0142255

99US-0142255

99US-0142920

99US-014354

99US-0144085

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99US-0144334

99US-0144335

99US-0144325

99US-0144335

99US-014433

99US-0144335

99US-0144325

99US-0145086

99US-0145087

99US-0145087

99US-0145088

99US-0145088
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99US-0137528

99US-0137528

99US-0137528

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99US-0138840

99US-013845

99US-0139452

99US-0139453

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99US-0135629.
99US-0136021.
99US-0136392.
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0.2 ANG 1999; 900 014700.
0.4 ANG 1999; 900 014700.
0.5 ANG 1999; 900 014700.
0.5 ANG 1999; 900 014700.
0.6 ANG 1999; 900 014700.
0.6 ANG 1999; 900 014700.
0.7 ANG 1999; 900 014700.
0.8 ANG 1999; 900
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RESULT 3
AAQ03999/c
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                                                                                                                                     QY
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 DEXXX
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                                                                                     RESULT
                                                                                                                                                            Query Match
Best Local S
Matches 19
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Best Local S
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ03999 standard; DNA; 877 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence complementary to dystrophin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ03999;
                                                                                                                                                                                                                        Paired oligonucleotide primers are used in detecting deletions specifically of the X and Y chromosomes. Dystrophin gene may be isolated this way.
                                                                                                                                                                                                                                                                                       \begin{array}{lll} \text{Multiplex genomic DNA amplification for deletion detection -} \\ \text{useful for detecting $x$-linked diseases such as ornithine} \\ \text{transcarbamylase deficiency and $x$-linked muscular dystrophy.} \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP364255-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        muscular dystrophy; dystrophin; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-chromosome; ornithine transcarbamylase deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGACTTCTGAGTAACAATCA 21
|||||||| ||| ||||||||
543 AAGACTTCAGAGTCACAATCA 563
                                                                                                                                                                                                                                                                                                                                                       CasKey CT,
                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-1988;
Arabidopsis thaliana DNA fragment SEQ ID NO: 66116.
                                                                                                                                                                                                     Sequence 877 BP; 289 A; 160 C; 131 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                   Claim 9; Page 19; 32pp; English.
                                                                                                                                                                                                                                                                                                                                  WPI; 1990-117752/16.
                                                                                                                                                                                                                                                                                                                                                                            (BAYU ) BAYLOR UNIV COLLEGE.
                      18-OCT-2000
                                           AAC50782;
                                                               AAC50782 standard; DNA; 1353 BP
                                                                                                                  Local Similarity
nes 19; Conserv
                                                                                                                                                            Local Similarity hes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                       Chamberlain JS, Gibbs RAL, Rainer JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                              Conservative
                      (first entry)
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99US-0161992.
99US-0161993.
99US-0162142.
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Pred. No. 56;
                                                                                                                                                                 0;
                                                                                                                                                                                   Score 17.8;
                                                                                                                                                                          Pred. No.
                                                                                                                                                                Mismatches
                                                                                                                                                                             56;
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                                                                                                                                                                                      DB 11;
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                                                                                                                                                                                     Length 877;
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0;

PR 23-JUN PR 29-JUN PR 29-JUN PR 30-JUN PR 30-JUN PR 30-JUN PR 01-JUN PR 01-JUN PR 00-JUN PR 10-JUN PR 11-JUN PR 12-JUN PR 12-JUN PR 12-JUN PR 12-JUN PR 21-JUN PR 21-	18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 21-JUN-1999; 22-JUN-1999;	18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999;	10-JUN-1999; 14-JUN-1999; 16-JUN-1999; 16-JUN-1999; 17-JUN-1999; 18-JUN-1999;	01-JUN-1999; 03-JUN-1999; 04-JUN-1999; 07-JUN-1999; 08-JUN-1999; 10-JUN-1999;	18-MAY-1999; 19-MAY-1999; 20-MAY-1999; 21-MAY-1999; 24-MAY-1999; 25-MAY-1999; 27-MAY-1999;	05-MAY 1999 06-MAY 1999 06-MAY 1999 07-MAY 1999 11-MAY 1999 14-MAY 1999 14-MAY 1999 14-MAY 1999 14-MAY 1999;	PR 08-APR-1999; 99US-0128234. PR 08-APR-1999; 99US-0128714. PR 16-APR-1999; 99US-012845. PR 21-APR-1999; 99US-0130077. PR 21-APR-1999; 99US-0130449. PR 23-APR-1999; 99US-0130891. PR 23-APR-1999; 99US-0130849. PR 33-APR-1999; 99US-0131449. PR 30-APR-1999; 99US-0131449. PR 30-APR-1999; 99US-0132404. PR 30-APR-1999; 99US-0132404.	25-FEB-1999 05-MAR-1999 05-MAR-1999 23-MAR-1999 23-MAR-1999 25-MAR-1999 29-MAR-1999	protein identification; simetabolic pathway; promote Arabidopsis thaliana. EP1033405-A2. 06-SEP-2000.

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RESULT 5
AAK54111/c
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29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
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13-SEP-1999;
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16-SEP-1999;
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22-SEP-1999;
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01-SEP-1999;
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13-OCT-1999;
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14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
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                Murine; liver; gene library; amino acid synthesis; binding protein; cell metabolism; energy metabolism; fatty acid metabolism; synthesis; phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide; replication; transcription; translation; transport protein; ss.
                                                              Murine transport and binding associated protein encoding cDNA SEQ ID
                                                                                   16-NOV-2001
                                                                                                                        AAK54111 standard; cDNA; 513
                                                                                                                                                                     543 AAGACTTCAGAGTCACAATCA 563
                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                       l Similarity
19; Conserv
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99US-0157865.
99US-0158029.
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99US-0160770
99US-0160814
99US-0160815
99US-0160980
99US-0160980
99US-0161404
99US-0161406
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99US-0160767.
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99US-0159637.
99US-0159638.
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99US-0151930.
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99US-0159294
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99US-0159330
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Pred. No. 59;
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RESULT 6
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel gene library (A) comprises a gene sequence (or its part) encoding a protein involved in amino acid synthesis, cellular/energy metabolism, metabolism of fatty acids/phospholipids, synthesis or breakdown of purines/pyrimidines/nucleosides/nucleotides, DNA replication/transcription/translation, or is a transport/binding protein. (A) are produced that correspond to the 3'-end of mRNA but without the polyA tail. They can be prepared more efficiently and with less effort than conventional libraries. AAK53436-AAK54275 represent fragments of the gene library described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene library containing sequences with specific 3'-ends and no polyA tail, encoding proteins involved in a wide range of cellular processes {\sf tail}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; Page 205-206; 251pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-368570/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                       ABL07736 standard; cDNA; 7626 BP
                                                                                                                                                                                                                                                                             prosophila; developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ ID NO 17690
                                                                                                                                                                                                                                                                                                                                                            ABL07736;
                                                                                                                                                                                                                                         Drosophila melanogaster
New isolated nucleic acid detection reagent for detecting 1000 or more
                           P-PSDB; ABB63633.
                                        WPI; 2001-656860/75.
                                                                    Venter JC, Adams M,
                                                                                          (PEKE ) PE CORP NY
                                                                                                                     23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                      27-SEP-2001.
                                                                                                                                                                                                                 WO200171042-A2
                                                                                                                                                                                                                                                                   pharmaceutical;
                                                                                                                                                                                                                                                                                                                                  26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 AAGATTTCTGGGTAACAATAAA 1
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86.4%;
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                                                                     PWD,
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sequences from the Coryneform bacterium Corynebacterium glutamicum. The sequences from the Coryneform bacterium corynebacterium glutamicum. The sequences from the formulation point of a gene derived from mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derifrom Coryneform bacterium, and identifying a homologue of a gene derifrom coryneform bacterium, and identifying a homologue of a gene derifrom coryneform bacterium, and identifying a homologue of a gene derifrom coryneform bacterium.
                                                                                                                                                                                                                                                                                   Nakagawa
Tateishi
                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                     The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                  WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-1999;
07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C glutamicum coding sequence fragment SEQ ID NO: 7064.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organic acid synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH68529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 17690; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ecification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                     SEQ ID NO: 7064; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                99JP-0377484.
2000JP-0159162.
2000JP-0280988.
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86.4%;
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RESULT 8
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              The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacla, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements
                                                                                                                                                                                                                                                                             New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                   Claim 1; Page 624; 747pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bzIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-мак-1999;
18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200053724-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pinus radiata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type 2 Cys2His2; CCAAT box element; MYB; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC57234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                              FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                McGrath A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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99US-0149485
                                                                                                                                                                                                                                                                                                                                                                                            Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.2%;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                           Glenn M;
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RESULT 9
ANK6626
AXX AAK6
XX AAK6
XX AAK6
XX Huma
DT 06-N
XX Huma
XX Huma
XX Huma
XX Homc
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Best Local Similarity 90.0
Matches 18; Conservative
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04-FEB-2000
24-FEB-2000
02-MAR-2000
16-MAR-2000
17-MAR-2000
17-MAR-2000
19-MAY-2000
07-JUN-2000
30-JUN-2000
07-JUL-2000
07-JUL-2000
07-JUL-2000
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Pred. No. 1.6e+02;
0; Mismatches 2;
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RESULT 10
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Complete acids into a host cell and culturing the cell to express the collagouse and treat immune/haematopoletic-related diseases, especially concers and cancer metastases of haematopoletic-derived cells. AAK64703 concers and cancer metastases.
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Best Local :
 Human immune/haematopoletic antigen genomic sequence SEQ ID NO:21437
                                    06-NOV-2001 (first entry)
                                                                                                                                                                    7221 AGCCTTCTGAGTACCAATCA 7240
                                                                                             AAK66625 standard; DNA; 21480 BP
                                                                                                                                                                                                                                                                              Sequence 21477 BP; 5311 A; 4999 C; 5256 G; 5911 T; 0 other;
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01-DEC-2000
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17-NOV-2000;
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18; Conservative
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2000US-0249300
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RESULT 11
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ID AAS01375/c
ID AAS013
XX AS013
AC AAS013
AC Human
XX Human;
KW Human;
KW INTERC
KW Gene t
KW 1ympho
KW 1ympho
KW autoim
XX Human;
CS Homo s.
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05-JAN-2001; 2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7222 AGCCTTCTGAGTACCAATCA 7241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS01375 standard; cDNA; 3114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; TANGO 210; clone jthLa152h06; TANGO 364; TANGO 366; dectin-2; INTERCEPT 394; INTERCEPT 400; TANGO 405; cellular process regulator; gene therapy; growth modulator; proliferation; cell differentiation; lymphocyte; bone marrow cell migration; leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TANGO 405 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS01375;
                                                                                                    mat_peptide
          WO200118016-A1
                                                                                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 76.4%;
Local Similarity 90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                           /*tag= 1
298..780
                                                                                                                                                                          /*tag= a
/product= "TANGO 405 protein"
/porte= "The ORF is specifically claimed"
154..297
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
154..783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encode the human immune/haematopoietic antigen (I) given in AAM82170 to AAM91921. (I) have cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
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Pred. No. 2.3e+02;
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RESULT 12
ABA18026
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local :
                                                                                                                                         Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
                       17-JAN-2001; 2001WO-US01334.
                                                                                                                    antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                16-AUG-2001.
                                                                      W0200159063-A2
                                                                                                          neurological disease; infection; nephrotropic; gene
                                                                                            HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                   1885 CTTCTGAGTATCAATCAA 1868
                                                                                                                                                                                                   Human nervous system related polynucleotide SEQ ID NO 10357.
                                                                                                                                                                                                                                  23-JAN-2002
                                                                                                                                                                                                                                                          ABA18026;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3114 BP; 1001 A; 527 C; 517 G; 1069 T; 0 other;
                                                                                                                                                                                                                                                                           ABA18026 standard; DNA; 29329 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecules encoding proteins useful as modulating agents in regulating a variety of cellular processes are used for treating e.g. cancer and autoimmune disorders -
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                                                                                                                                                                                                                                                                                                                                                       5 CTTCTGAGTAACAATCAA 22
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                                                                                                                                                                                                                              (first entry)
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Pred. No. 36
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                                                                                                         therapy; vaccine;
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21-SEP-2000;
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26-SEP-2000;
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23-AUG-2000;
30-AUG-2000;
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18-AUG-2000;
22-AUG-2000;
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12-SEP-2000;
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08-SEP-2000;
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06-SEP-2000;
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04-FEB-2000;
24-FEB-2000;
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14-AUG-2000;
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19-MAY-2000;
                                         2000US-0234998
2000US-0235484
2000US-0235834
2000US-0235834
2000US-0236337
2000US-0236367
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2000US-0232399.
2000US-0232400.
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2000US-0231968.
2000US-0232397.
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2000US-0229345.
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2000US-0220964.
2000US-0224518.
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2000US-0215135
2000US-0216647
2000US-0216880
2000US-0217487
2000US-0217496
2000US-0217496
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2000US-0234223
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2000US-0180628.
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2000US-0190076.
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01-NOV-2000;
08-NOV-2000;
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02-OCT-2000;
02-OCT-2000;
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useful for preventing, cancers and metastases
            Nucleic acids encoding 3224 human nervous system antigen polypeptides,
                                                                                                                                                                                                                                                  17-NOV-2000;
                                                            (HUMA-) HUMAN GENOME SCI INC.
                                              Barash SC,
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2000US-0237038.
2000US-0237039.
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2000US-0239937
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2000US-0249216.
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2000US-0246477
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      diagnosing and/or treating nervous system
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ACX XXX ACT DIT TO REPORT 
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                            18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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8110 GACTTCTGAGAAACAATC 8127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; cardiant; immune disorder; cardiovascular disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nervous system related polynucleotide SEQ ID NO 12842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurological disease; infection; nephrotropic; gene therapy;
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                                                                                                                                             2000US-0198123.
2000US-0205515.
2000US-0209467.
                                                           2000US-0214886.
2000US-0215135.
2000US-0216647.
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2000US-0189874
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Pred. No. 3.
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2000US-0217496. 2000US-0218290. 2000US-0220963. 2000US-0220964. 2000US-0224518.

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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune harmolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease multina autoimmune thyroiditis, autoimmune controlled.
                                                                                                                                                                                                                                                                                                                                             17-NOV-2000

11-NOV-2000

01-DEC-2000

01-DEC-2000

05-DEC-2000

05-DEC-2000

06-DEC-2000

06-DEC-2000

08-DEC-2000

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08-DEC-2000
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08-NOV-2000
08-NOV-2000
08-NOV-2000
17-NOV-2000
                                                                                                                                                                                         Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                                                                                                                                                               Disclosure; SEQ ID NO 12842; 1701pp +
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08-NOV-2000;
08-NOV-2000;
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08-NOV-2000

08-NOV-2000

08-NOV-2000

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08-NOV-2000

08-NOV-2000
                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                   2001-541565/60
        multiple
                                                                                                                                                                                                                                                                            Barash SC,
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2000US-0246476.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246523.
2000US-0246523.
2000US-0246523.
2000US-0246523.
2000US-024663.
2000US-0246611.
2000US-024661.
2000US-024661.
2000US-024920.
2000US-024920.
2000US-024921.
2000US-02492.
2000US-0251.66.
2000US-0251.66.
2000US-0251.86.
sclerosis, rheumatoid arthritis and ulcerative
                                                                                                                                                                                                                                                                           Ruben
                                                                                                                                                             Sequence Listing; English.
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2000US-0232397. 2000US-0232398. 2000US-0232399. 2000US-0232401. 2000US-0232401. 2000US-0233063. 2000US-0233064. 2000US-0233064. 2000US-0233064.

14-AUG-2000 18-AUG-2000 22-AUG-2000 22-AUG-2000 23-AUG-2000 30-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 14-SEP-2000 14-SEP-2000

2000US-0226279 2000US-0226681 2000US-0226868 2000US-0226868 2000US-0227182 2000US-022909 2000US-0229287 2000US-0229287 2000US-0229287 2000US-0229343 2000US-0229345 2000US-0229345 2000US-0229345 2000US-0229513 2000US-0229513 2000US-0239437

14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 20-OCT-2000 20-OCT-2000

2000US-0240960. 2000US-0241785. 2000US-0241786. 2000US-0241787. 2000US-0241808.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                        28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                              31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-MAR-2000;
19-MAY-2000;
07-UUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK70791 standard; DNA; 29329 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK70791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2001; 2001WO-US01354.
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2000US-0190076
2000US-0198123
2000US-0205515
2000US-0209467
                           2000US - 0214886.
2000US - 0215135.
2000US - 0216880.
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2000US - 0217487.
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2000US - 0225214.
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2000US - 022526.
2000US - 022526.
2000US - 022527.
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94.4%;
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Pred. No. 3.6e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
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          22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
         29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-CCT-2000;
02-CCT-2000;
03-CCT-2000;
04-NOV-2000;
08-NOV-2000;
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25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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06-SEP-2000;
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21-SEP-2000;
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12-SEP-2000;
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2000US-0230438
2000US-0231243
2000US-0231243
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2000US-0231411
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2000US-0233081
2000US-0233081
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2000US-023299
2000US-023499
2000US-0234997
2000US-0234997
2000US-0234997
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2000US-0234997
2000US-0234997
2000US-0234997
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2000US-0235834
2000US-0235834
2000US-0235834
2000US-0235834
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2000US - 0236368

2000US - 0236369

2000US - 0236802

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2000US - 0239035

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2000US - 0241786

2000US - 0241787

2000US - 0241787

2000US - 0246476

2000US - 0246476
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2000US-0229509
            2000US-0246528
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2000US-0246613
2000US-0249207
2000US-0249208
                                                                                                                            2000US-0246524.
2000US-0246525.
2000US-0246526.
2000US-0246527.
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2000US-0227009
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AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC expension, they may be used to treat disorders associated with decreased CC expension by rectifying mutations or deletions in a patient's genome CC expression by rectifying mutations or deletions in a patient's genome CC expression by rettifying mutations or deletions in a patient's genome CC expression by rettifying mutations or deletions in a patient's genome CC expression by rettifying mutations or deletions in a patient's genome CC expression by rettifying for the produce the activity of (I) by expressing inactive proteins or to CC polynucleotides may be used to produce the secreted (I), by inserting CC contein (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially concers and cancer metastases of haematopoietic antigen genomic represent sequences from the present invention. AAK54942 to AAK94950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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                                   á
                                                                                Query Match
Best Local :
                                                                 Matches
8110 GACTTCTGAGAAACAATC 8127
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01-DEC-2000
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05-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
                                                                                                                   Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 25603; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoletic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000;
17-NOV-2000;
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                            3 GACTTCTGAGTAACAATC 20
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                                                                 1 Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC,
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0249218.
2000US-0249244.
2000US-0249245.
2000US-0249264.
2000US-0249265.
2000US-0249265.
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2000US-0251989
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2000US-0256719.
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                                                                         74.5%; Score 16.4; DB 22; 94.4%; Pred. No. 3.6e+02;
                                                              0
                                                              Mismatches
                                                          Indels
                                                                                       Length 29329;
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AAK78512
XXX

XXX

AAC
AAK7
XXX

AC
AAK7
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Huma
XXX

Homo
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Homo
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Homo
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Homo
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Homo
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Hom
XX

22-AUG-2000)
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30-AUG-2000)
01-SEP-2000)
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11-SEP-2000)
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14 - AUG - 2000)
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22-AUG-2000;
22-AUG-2000;
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26-JUL-2000;
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17-MAR-2000;
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2000US-0217487
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2000US-0225270.
2000US-0225447.
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2000US-0225266.
2000US-0225267.
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2000US-0225213.
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2000US-0229287
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2000US-0220963
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Gaps

0;

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29-SEP-2000;
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29-SEP-2000;
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20-CCT-2000;
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03-NOV-2000;
04-NOV-2000;
08-NOV-2000;
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25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
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21-SEP-2000;
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2000US-0235836.

2000US-0236327.

2000US-0236367.

2000US-0236368.

2000US-0236368.

2000US-0236370.

2000US-0236370.

2000US-0236802.

2000US-0236802.
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2000US - 0233063.
2000US - 0233064.
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2000US - 0234274.
2000US - 0234274.
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2000US-0246474
2000US-0246475
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2000US-0232399
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2000US-0249216.
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2000US-0249217.
2000US-0249244.
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2000US-0246532.
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2000US-0246610.
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2000US-0235484.
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2000US-0241787.
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2000US-0246527.
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AA AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cartivity, and can be used in gene therapy and vaccine production. (I) CC activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and cc example, they may be used to treat disorders associated with decreased CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC supplement the patients own produce the secreted (I), by inserting CC polynucleotides may be used to produce the secreted (I), by inserting CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC cancers and cancer metastases of haematopoietic antigen genomic to AAK87994 represent invention. AAK54942 to AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
                                                                          Matches
                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 33324; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483426/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                             Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
Local
                                   3 GACTTCTGAGTAACAATC 20
                                                                          17; Conservative
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2000US-0251479.

2000US-0251479.

2000US-0251856.

2000US-0251868.

2000US-0251869.

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2000US-0251999.
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                                                                                              74.5%;
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                                                                              0;
                                                                                                Score 16.4; DB 22
Pred. No. 3.6e+02;
                                                                                Mismatches
                                                                                                                   DB 22;
                                                                                                                   Length 29329;
                                                                                    0;
                                                                                      Gaps
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Search completed: March 17, 2003, 10:52:21 Job time : 217.253 secs

Дb

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               March 17, 2003, 10:23:12; Search time 777.688 Seconds (without alignments) 458.154 Million cell updates/sec
    US-09-836-439-6
22
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em_estpl::
em_estro::
em_htc::
gb_est1::
gb_est3::
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em_estfun:*
em_estfun:*
em_estfun:*
gb_gss:*
em_gss_hum:*
em_gss_hum:*
em_gss_pln:*
em_gss_fun:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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o	. US #	·ω	N	ь	Result
17.8	17.8	17.8	18.4	18.4	Score
80.9	80.9	80.9	83.6	83.6	Query
545	509	364	395	347	Query Match Length DB ID
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AI738689	BG882650	AA229942	AA837289	AA970603	esult Query NO. Score Match Length DB ID
AI738689 wi22a08.x	BQ622226 fchlc.pk0 BG882650 sae94q07.	AA229942 nc51h06.r	AA837289 od26e07.s	AA970603 op40f09.s	Description

ALIGNMENTS

FEATURES source	JOURNAL COMMENT	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AA970603/c LOCUS DEFINITION
Insert Length: 1053 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 344. Location/Qualifiers 1347 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1579337"	Index to the lines of the following problems	Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 347) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		AA970603 347 bp mRNA linear EST 07-JUL-1998 op40f09.sl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone

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Query Match
                                                                                                                                                                                                                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GACTTCTGAGTAACAATCAA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 395)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     od26e07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1369092,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                       /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
/clone="IMAGE:1369092"
/clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                   /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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95.0%;
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Pred. No. 4.1e+02;
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COMMENT

JOURNAL

REFERENCE

TITLE

AUTHORS

SOURCE KEYWORDS ACCESSION /ERSION

ORGANISM

FEATURES

Matches

Conservative

0;

Mismatches

Indels

0;

Gaps

0,

Best Local Similarity

RESULT 2 AA837289/c

DEFINITION

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Matches

BASE COUNT

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BASE COUNT
ORIGIN
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                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
fissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.,
Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 616 Std Error: 0.00
seq primer: -28m13 rev1 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 364) NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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similar to contains Alu repetitive element;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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                                                                                                                                              /note="Vector: pamp10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10 000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constructed by Bento Soares and M. Fatima Bonaldo."

<sub>1</sub> 77 c 73 g 145 t
                                                                                                     library was constructed by David Krizman."
82 c 86 g 95 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1011707"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_Pr3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:1852255
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95.0%;
     90.5%;
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Score 17.8; DB 9;
Pred. No. 7.9e+02;
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Pred. No. 4.3e+02;
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                            DB 9;
                            Length 364;
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         TITLE
                                                                                                                                     AUTHORS
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         Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna, A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schur,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoldeae; Phaseoleae;
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                          sae94g07.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1065-3758 5', mRNA sequence.
                                                                                                                                                                                                                                                             Glycine max
                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                          BG882650.1 GI:14259742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Entomology University of Maryland 4112 Plant Sciences Building, College Park, MD 20742, USA Tel: 301 405 16 13 Fax: 301 314 92 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungl; Zygomycota; Zygomycetes; Entomophthorales; Ancyllataceae; Conidiobolus.

1 (bases I to 418)
Freimoser, F. M., Screen, S., Hu. G. and St. Leger, R. J.
EST analysis of genes expressed by the zygomycete pathogen Conidiobolus coronatus during optimized secretion of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Freimoser F. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
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                                                                                                                                                     (bases 1 to 509)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ff34@umail.umd.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:31488"
/dlowellb="Conidiobolus cornatus ARSEF 512"
/clone_llb="Conidiobolus cornatus was grown in mote="Vector: Unizap; Conidiobolus coronatus was grown in minimal medium supplemented with Manduca sexta cuticle and peptone for 18 hours. A cDNA library was constructed in the unidirectional Lambda vector Unizap."

85 c 76 g 136 t 2 others
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90.5%;
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Pred. No. 8.3e+02;
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                                                                                                   Beck, C.,
                                                                                                                     Khanna
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGACTTCTGAGTAACAATCAA 22
                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
               CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI738689 mRNA linear wi22a08.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMA similar to TR:054729 054729 BRAIN. ;, mRNA sequence.
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                    Tumor Gene Index
                                                                                                                                                                                                                                                                                            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 545)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhOI; The cDNA library was constructed from mRNA isolated germinating shoots of the cultivar williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhOI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhOI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhOI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GlbcoBRL). This library was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shoemaker."
1 91 c
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/clone="CENOME SYSTEMS CLONE ID: Gm-c1065-3758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="germinating shoots"
/lab_host="DH10B"
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Pred. No. 8.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vk55a10.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone TMAGE:958554 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaiia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA546700.1 GI:2307991
                                                                                                                                                                                                                                                        High quality sequence stop: 405
                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                          mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECC RI; Plasmid DNA from the normalized library NCL_CGAP_Col0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo. "a 131 c 82 g 167 t
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Col6"
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/clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript Si
                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
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Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bjloftus@tigr.org
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                                                                                                                                                                                                                                                                                                            /Clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: BSt I; Constructed at The
/note="Vector: pHOS1; Site_1: BSt I; Constructed at The
/note="Vector: pHOS1; Site_1: Constructed at The
/note="Vector: pHOS1; Site_1: Constructed at TIGR), Rockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Institute for Genomic Construction Bst I; Constructed for Isolate identification.

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/strain="HM1:IMSS"
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                                 Score 17.8; DB 17
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509 AAGACTTCTTTGTAACAATCA 489

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ORIGIN
                                                                                                                   KEYWORDS
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TITLE
                                                                       ORGANISM
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EST.
Physcomitrella patens.
Physcomitrella patens
Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                              gb06f02.yl Moss EST library PPN Physcomitrella patens cDNA clone PEP_SOURCE_ID:PPN080304 5' similar to TR:Q96538 Q96538 ACYL-COA
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                                                                                                                                                                                                                                                               AW699516
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Tel: 919 515 7800
Fax: 919 515 7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Johnson, Arthur
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                                                                                                                                           AW699516.1 GI:7583607
                                                                                                                                                                       AW699516
                                                                                                                                                                                     SYNTHETASE ; , mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11: ajohnson@unity.ncsu.edu
primer: T3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab.host-"XLI-Blue"

//lab.host-"XLI-Blue"

//note-"Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI

/ The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. oligo-dT primed cDNA
was directionally cloned into the EcoRI-XhoI BlueScript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCACGAG'."

80 a 76 c 76 g 129 t 14 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="nxSI_053_A10"
/clone_lib="nxSI (Nsf Xylem Side wood Inclined)"
/tissue_type="Xylem"
/cell_type="Side"
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94.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17.4; DB 12
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                               474 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                            linear
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Pinus; Pinus.
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COMMENT
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                                                                                                                                                                                                                                    ACTICIGAGIAACCATCAA 414
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,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood
,K., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T.,
$teptoe,M., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.
Waterston,R. and Wilson,R.
NXSI_108_D07_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA clone NXSI_108_D07 5', mRNA sequence.
                                                                    BG040453
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Libraries were constructed by Dr. Stavros Bashlardes as part of the
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Seq_primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leeds/Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Location/Qualifiers
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: Thote="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: Thote="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: Thote-was constructed using an oligo dT primer/linker that contains a XhoI site within it. Following ds cDNA synthesis, EcoRI adapters with XhoI. The result is cDNA synthesis, EcoRI adapters were ligated to the blunt ends and sample was digested with XhoI. The result is cDNA with an EcoRI sticky end on one side and a XhoI sticky end on the other. This cDNA was ligated directionally in UnizAp arms. The vector is designed containing the pBluescript sequence as well as lambda DNA and cDNA is cloned within this pBluescript sequence. The vector was then packaged using Gold giapackaging extracts. Library was grown in XIIBlue MRF, cells and amplified. The library was grown in XIIBlue exassist as a helper phage that releases the pBluescript sequence and circularises it as single stranded plasmids that are then packaged (by helper phage) and secreted out of the host cell as phagemids. SOLR cells were transformed with phagemids and the library was plated out on LB-amp plates to select for transformants. Approximately 1,000,000 colonies were grown and recovered by using Oulagen transform DH10B cells by electroporation."
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/clone_lib="Moss EST library PPN"
/tlssue_type="protonemata: 7 day old tissue auxin treated"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Physcomitrella patens"
/db_xref="taxon:3218"
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94.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.4; DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.3e+03;
                                                                477 bp
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 474;
                                                                    linear
                                                                    EST 24-JAN-2001
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RESULT 12
AW738913/c
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                      JOURNAL
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                                                                Physcomitrella patens.
Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Eukaryota; Viridiplantae; Funariales; Funariaceae; Physcomitrella.
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 549)
1 (bases 1 to 549)
1 (bases 1 to 549)
1 (bases 1, Bashiardes, S., Cove, D., Cuming, A., Knight, C., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Watterston, R. and Wilson, R., Waterston, R. and Wilson, R.
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Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW738913

549 bp mRNA linear EST 25-APR-2000 gb16b06.yl Moss EST library PPN Physcomitrella patens cDNA clone PEP_SOURCE_ID:PPN100912 5' similar to TR:Q96538 Q96538 ACYL-COA
                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                     AW738913.1 GI:7647930 EST.
                                                                                                                                                                                                                                                                                                                                                                                                          SYNTHETASE ;, mRNA sequence. AW738913
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1 (bases 1 to 477)
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                                                  Leeds/Wash U Moss EST Project
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//lab_host="XL1-Blue"
//lab_host="XL1-Blue"
//lab_host="XL1-Blue"
//note="vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library, oligo-dT primed cDNA
was directionally cloned into the EcoRI-XhoI BlueScript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCACGAG'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:352"
/clone="NXSI_108_D07"
/clone="NXSI_108_D07"
/clone_lib="NXSI (Nsf xylem Side wood Inclined)"
/tissue_type="xylem"
/cell_type="Side"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.18;
94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.4; DB 12
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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RESULT 13
AQ525332
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                                                               REFERENCE
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Best Local S
Matches 18
                               AUTHORS
                                                                                                                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 ACTTCTGAGTAACCATCAA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ACTTCTGAGTAACAATCAA 22
                                                                                                                                                                                                                                                                                                       AQ525332 608 bp DNA linear GSS 11-MAY: HS_5226_B1_C08_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=802 Col=15 Row=F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Libraries were constructed by Dr. Stavros Bashiardes as part of the Physcomitrella EST program (PBP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a close please contact: Celia Knight (c.d.knight@leeds.ac.uk)
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 608)
Mahairas,G.G., Wallace,J.C.,
Keller,A., Shaker,R., Furlon
                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                 AQ525332.1
                                                                                                                                                                                                                                                                              AQ525332
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Construction of the cDNA library was carried out using Stratagenes 'UniZAP - CDNA synthesis kit'. CDNA was constructed using an oligo dT primer/linker that contains a XhoI site within it. Following ds cDNA synthesis, EcoRI adapters were ligated to the blunt ends and sample was digested with XhoI. The result is cDNA with an EcoRI sticky end on one side and a XhoI sticky end on the other. This cDNA was ligated directionally in UniZAP arms. The vector is designed containing the pBluescript sequence as well as lambda DNA and cDNA is cloned within this pBluescript sequence. The vector was then packaged using Gold gigapackaging extracts. Library was grown in XLIBlue MRF' cells and amplified. The library was sexcised by mass excision using Stratagens 'Mass excised kit' that uses exassist as a helper phage that releases the pBluescript sequence and circularises it as single stranded plasmids that are then packaged (by helper phage) and secreted out of the host cell as phagemids. SOLR cells were transformed with phagemids and the library was plated out on LB-amp plates to select for transformants. Approximately 1,000 clonies were grown and recovered. The double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,000 colonies were grown and recovered. The double stranded plasmid library was recovered by using Quiagen Midi prep kit. 2 micro grams of each library were used to transform bH10B cells by electroporation."

a 116 c 125 g 157 t
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/clone_11b="Moss EST library PPN"
/tissue_type="protonemata: 7 day old tissue auxin treated"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Physcomitrella patens"
/db_xref="taxon:3218"
                                                                                                                                                                                                                                                 GI:4772652
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94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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Pred. No. 1.4e+03;
Smith, K., Swartzell, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           St. Louis, MO 63108, USA
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Holzman,T.,
Adams,M.D.
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Furlong, J.,

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SOURCE
ORGANISM
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BJ173371
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                                                                                                                                                       COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 79.1%;
Local Similarity 85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAGACTTCTGAGTAACAATCA 21
                    Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855
                                                                                                                                                                                                                                                                                     Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funarildae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 611)
Fujita,T., Shin.1,T., Seki,M., Kamiya,A., Ochiyama,I., Nishiyam
                                                                                                                                                                                                       Comparison of the moss Physcomitrella patens genome with flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BJ173371 611 bp mRNA linear EST 24-BJ173371 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone pph35g12 3', mRNA sequence.
BJ173371
Email: tshini@genes.nig.ac.jp
                                                                                                                                               Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                             plants genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BJ173371.1 GI:18341336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library availability, please contact Pleter de Jong (Pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 802 row: F column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: jwallace@u.washington.edu
Clones are derived from the human BAC_library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                                                                                                                                                                                                                                    jita,T., Shin-1,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.
Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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BJ171523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                           Email: tslini@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified lPS phage vector (Mo bi Tec, Germany). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector. cDNA instert could tail was ligated to DanmHI site of the vector. This full-length amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al.
Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BJ171523 692 bp mRNA linear EST 24 CBJ171523 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
Contact: Tadasu Shin-i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 692)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified lPS phage vector (Mo bi Tec, Germany). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector. cDNA instert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light.
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/organism="Physcomitrella patens subsp. patens
/db_xref="taxon:145481"
                                                                 1. .692
                                                                                        Location/Qualifiers
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gametophores with 2 to 5 leaves"
1 135 c 128 g 170 t
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/db_xref="taxon:145481"
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94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 611;
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